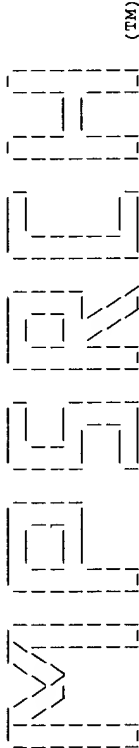


\*\*\*\*\*2\*\*\*\*\*



(TM)

\*\*\*\*\*2\*\*\*\*\*

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:56:03 1999; MasPar time 28.46 Seconds  
411.665 Million cell updates/sec

Tabular output not generated.

Title: >US-09-026-400-4  
Description: (1-551) from US09026400.pep  
Perfect Score: 3749  
Sequence: 1 MATVRQSDGVAANGLAFAAA.....LGRKSFQQRNKRNSDDC 551

Scoring table: PAM 150  
Gap 11

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39

Statistics: Mean 35.992; Variance 182.932; scale 0.197

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3749	100.0	551	34	Nicotianamine aminotr	2.58e-301
2	2888	77.0	461	34	Nicotianamine aminotr	1.97e-228
3	402	10.7	394	26	Aquifex aspartate ami	3.44e-21
4	269	7.2	398	26	Ammonifex degensli as	7.20e-11
5	259	6.9	373	26	Aquifex aspartate ami	4.11e-10
6	230	6.1	482	26	Barley alanine aminot	6.10e-08
7	229	6.1	517	20	Carnation ACC synthas	7.24e-08
8	213	5.7	422	17	Human kynurenine amin	1.10e-06
9	207	5.5	423	17	Rat kynurenine aminot	3.02e-06
10	207	5.5	437	17	Rat kynurenine aminot	3.02e-06
11	207	5.5	457	17	Rat kynurenine aminot	3.02e-06
12	196	5.2	493	5	ACC synthetase.	1.90e-05
13	186	5.0	175	2	Peptide antigenic for	9.99e-05
14	189	5.0	429	1	Antigenic protein for	6.08e-05
15	186	5.0	486	23	Poplar 1-aminocyclopr	9.99e-05
16	186	5.0	493	29	Zucchini ACC synthase	9.99e-05

17	186	5.0	493	3	RJ5505	Zucchini ACC synthase	9.99e-05
18	187	5.0	496	7	R35231	Rat ALT.	8.47e-05
19	185	4.9	493	29	W47310	Protein encoded by zu	1.18e-04
20	185	4.9	493	3	R15504	Zucchini ACC synthase	1.18e-04
21	180	4.8	936	39	W89801	Staphylococcus aureus	2.68e-04
22	175	4.7	480	32	W60239	Rose 1-aminocycloprop	6.07e-04
23	177	4.7	494	29	W47312	Zucchini ACC synthase	4.38e-04
24	177	4.7	494	3	R15863	Zucchini ACC synthase	4.38e-04
25	171	4.6	362	20	W04559	Carnation ACC synthas	1.16e-03
26	171	4.6	493	7	R35230	Human ALT.	1.16e-03
27	172	4.6	495	30	W46904	A human mutant alanin	9.90e-04
28	172	4.6	496	34	W62267	Modified human alanin	9.90e-04
29	167	4.5	469	3	R15510	Tomato ACC synthase e	2.23e-03
30	168	4.5	980	14	R81318	Adhesion protein.	1.89e-03
31	167	4.5	1059	1	P82962	SEPI4 protein compris	2.23e-03
32	170	4.5	1092	29	W41602	Staphylococcus epide	1.37e-03
33	166	4.4	402	2	P70709	Plasmodium cynomolgi	2.62e-03
34	164	4.4	1038	19	R95107	Fibronectin cell bind	3.61e-03
35	161	4.3	481	23	W21754	Poplar 1-aminocyclopr	5.85e-03
36	160	4.3	695	31	W53526	Amino acid sequence o	6.87e-03
37	161	4.3	1023	31	W53524	Amino acid sequence o	5.85e-03
38	161	4.3	1059	8	R41013	SLP4 multimeric prote	5.85e-03
39	161	4.3	1059	24	W26348	SLP4 synthetic protei	5.85e-03
40	163	4.3	1177	24	W26342	Silk-like protein Slp	4.24e-03
41	163	4.3	1177	1	P80940	SLPiii protein compri	4.24e-03
42	163	4.3	1177	19	R95105	Silk like protein (SL	4.24e-03
43	163	4.3	1177	1	R05307	SLP III (Silk-fibroin	4.24e-03
44	163	4.3	1178	32	W53518	Amino acid sequence o	4.24e-03
45	163	4.3	1178	8	R41007	Silk-like protein Slp	4.24e-03

ALIGNMENTS

RESULT 1  
ID W61643 standard; Protein; 551 AA.  
AC W61643.  
DT 27-OCT-1998 (first entry)  
DE Nicotianamine aminotransferase 58148.62 molecular weight protein.  
KW Nicotianamine aminotransferase; plant; iron absorption;  
OS Gramineae sp.  
PN EP-860499-A2.  
PD 26-AUG-1998.  
PR 19-FEB-1998; 102891.  
PF 21-FEB-1997; JP-037499.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
PI Mori S, Nakanishi H, Takahashi M;  
DR WPI: 98-439341/38.  
DR N-PSDB; V48148.  
PT New nicotianamine aminotransferase protein and DNA - useful for  
PT enhancing iron absorption of plant cells  
PS Claim 3; Page 14-15; 17pp; English.  
CC The nicotianamine aminotransferase can be used in a plasmid to transform  
CC plant cells to produce cells with enhanced iron absorption, and it is  
CC implied [though not stated] that plants with improved resistance to iron  
CC deficiency chlorosis in calcareous soils can be regenerated from the  
CC transformed cells. The gene fragment can be used to detect, amplify  
CC and/or isolate nicotianamine aminotransferase genes.  
SQ Sequence 551 AA;  
Query Match 100.0%; Score 3749; DB 34; Length 551;  
Best Local Similarity 100.0%; Pred. No. 2.58e-301;  
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	matvrqsdgvaanglavaaaangksnghgvaavngksnghgvdadangkngghvaada	60
QY	1	MATVRQSDGVAANGLAFAAAANGKSNHGHVAAVNGKSNHGHVDAADANGKNGHGAADA	60
Db	61	ngksnghaeatgheatangktngtrhresnghaeaaadangesnehaedsaangesnha	120
QY	61	NGKSNHAEATANGHEATANGKTNGHRESNGHAEAAADANGESNEHAEDSAANGESNHA	120
Db	121	aaaaaeaeavnfagadgvlaatganmsirairkyiasvqekgprviplahgdpsv	180

Qy	121	AAAAEEBAEVEWNPAGAKDGVLAATGANMSIRAIRYKISASVOEKGRPVLPPLAHGDP5V	180
Db	181	fpafirtaveaedavaaavrtggfncypagvqlpaarsavaehlsqgvpymlsaddvflta	240
Qy	181	FPAFTAVEAEDAFAAVRTGQFNCPYAGVGLPAPARSVAEHLUSQGVYMLSADDVFLTA	240
Db	241	gggtqaieviipvlaqtaganillprpgypnyearaafnrlevrhfdltpdkgweidisl	300
Qy	241	GGTQAEIIVIPVLAQTAGANILLPRPGYPNYEARAANRLEVRHFDLIPDKGWEIDISL	300
Db	301	esiadknttamviinpnpcgsvsyshlskvaevakrjilviadevvgkvlvgsapfi	360
Qy	301	ESTADKNTTAMVIINPNPCGSVSYDHLKSVAEAKRJILVIADENVYVKLVGSAPFI	360
Db	361	pmgvfghitpvlslgslskswipwgrlgwavydprkllqekistsitnylnvstdpa	420
Qy	361	PMGVFGHITPVLSTGSLSKSWIVPGRWLGWAYDPRKLLQETKISTSTNYLNSTDPA	420
Db	421	tfiqaalpqlentkedffkaiiglklkesseicykikenkyitcphkpegsmfvmvkl	480
Qy	421	TFIOAAPQLILENTKEDFFKAIIGLKLKESSEICYKIKENKYITCCHKPEGSMFVMVKLN	480
Db	481	lhleeiddiddfccklakeesvilcpvgslgmanvwriftacvpssldgqigrklsfcq	540
Qy	481	LHLEEIDDDIDDFCCKLAKEESVILCPGVSILGMANVWRIFTACVPSSLDQGLGRKLSFCQ	540
Db	541	rnkkrnsddc	551
Qy	541	RNKKRNSDDC	551

RESULT 2

ID W61642 standard; Protein; 461 AA.  
AC W61642;  
DT 27-OCT-1998 (first entry)  
DE Nicotianamine aminotransferase 49564.15 molecular weight protein.  
KW nicotianamine aminotransferase; plant; iron absorption;  
KW iron deficiency chlorosis.  
OS Gramineae sp.  
PN EP-860499-A2.  
PN 26-AUG-1998.  
PD 19-FEB-1998; 102891.  
PF 21-FEB-1997; JP-037499.  
PR (SUMO ) SUMITOMO CHEM CO LTD.  
PI Mori S, Nakanishi H, Takahashi M;  
DR WPI; 98-439341/38.  
DR N-PSDB; V48147.  
PT New nicotianamine aminotransferase protein and DNA - useful for  
PT enhancing iron absorption of plant cells  
PS Claim 3; Page 12-13; 17pp; English.  
CC The nicotianamine aminotransferase can be used in a plasmid to transform  
CC plant cells to produce cells with enhanced iron absorption, and it is  
CC implied [though not stated] that plants with improved resistance to iron  
CC deficiency chlorosis in calcareous soils can be regenerated from the  
CC transformed cells. The gene fragment can be used to detect, amplify  
CC and/or isolate nicotianamine aminotransferase genes.  
SQ Sequence 461 AA;  
SQ

```

Query Match      77.0%; Score 2888; DB 34; Length 461;
Best Local Similarity 88.1%; Pred. No. 1,97e-228;
Matches 409; Conservative 30; Mismatches 20; Indels 5; Gaps 1;

Db 3 hgshgheaaaaaangksnghaaaaangksnghaaaaa-----vwnfarkgdkgillatga 57
      :|||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 88 RESNGHAERADANGESNEHAEDSAANGSNGHAAAAAEEEEAVEWNFAGKDGVLAAATGA 147

Db 58 knsirairyKisaveesgprpvlplahgdpvfpafrtaveaedavaaalrtgqfncya 117
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 148 NMSIRAIRYKISASVQEKGRPVLPLAHGDPSPVFPAPRTAVEAEDAVAAAVRTGFNCYP 207

Db 118 agvglpaarsavaehlsqgpyklsaddvfltaggtqtaievlpvlaqtaganillprpg 177
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

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Qy	208	AGVGLPAARSVAEHL	SQGVYPML	SADDVFLTAGG	QTAIEVILPVL	AQTAGANILL	PRPG	267		
Db	178	ypnyeaaafnklevr	hfdlfpk	gweidsls	tsiadkntt	amvinpnpcgsvsyd	237			
Qy	268	YPNYEAAAFNRLEVR	FDLIPK	GWEDIDSL	ESTADKNTT	AMVINPNPCGSVSYD	327			
Db	238	hlakvaevar	klgilviade	vygklvl	lgsapfip	mgvfg	hiapvls	lsgslks	swipgwr	297
Qy	328	HLSKVAEYAKRLG	TLVTADE	VYKLVLS	APFIPMG	VFGHITP	VLSTGSL	SKSWIPGWR	387	
Db	298	lgwvavdpt	kilekktk	istsitny	lnvstdp	atfvgeal	pkilentka	dfkfr	iiigllk	357
Qy	388	LGWAVVDPRK	LQETKIS	ISITNLYN	VSDPTATF	IQALPQ	ILENTKED	FFRAII	IGLLK	447
Db	358	esseicyreiken	kyitcphk	pegsfmv	kmklhl	leeihdd	idfcck	lakees	vilcp	417
Qy	448	ESSEICYKIQEN	KYITC	PHKPEGS	MFVMVKL	NHLLEE	IDDDID	DFCK	LAKEES	507
Db	418	gsvlgnmwn	writfac	vpslqdg	lervksf	cqrnkk	ksinsgc	461		
Qy	508	GSVLGMANW	RITFAC	VPSSLQD	LGRLK	IFCQRNKK	RNSDDC	551		
RESULT 3										
ID	W24257	standard; Protein; 394 AA.								
AC	W24257	18-FEB-1998 (first entry)								
DE	Aquifex	aspartate aminotransferase VF5/AA.								
KW	Aspartate	aminotransferase; VF5/AA; chiral compound.								
OS	Aquifex	sp. strain VF5.								
PN	W09729	187-AJ.								
PD	14-AUG-1997.									
PF	21-JAN-1997;	U01094.								
PR	08-MAY-1996;	US-648590.								
PR	09-FEB-1996;	US-599171.								
PA	(RECO-)	RECOMBINANT BIOCATALYSIS INC.								
PI	Swanson	RV, Warren PV;								
DR	WPI:	97-415343/38.								
DR	N-PSDB;	T78781.								
PT	New	transaminase(s) and aminotransferase(s) derived from host cells								
PT	-	used for producing enzymes, and hybridisation probes for a cDNA or								
PT	genomic	library								
PS	Claim	19; Fig 10; 95pp; English.								
CC	This	protein sequence comprises aspartate aminotransferase VF5/AA								
CC	of	Aquifex VF5, a strictly chemolithoautotrophic marine eubacterium								
CC	which	grows optimally at 85-90 deg C and pH 6.8 in high salt								
CC	medium.	The VF5/AA amino acid sequence was deduced from genomic								
CC	DNA (see	T78781). Claimed thermostable transaminases and								
CC	aminotransferases	(W24248-57) can be produced from native or								
CC	recombinant	host cells for use with L- and/or D-amino acids for								
CC	production	of optically pure chiral compounds used in the								
CC	pharmaceutical,	agricultural and other industries. A method is								
CC	claimed	for transferring an amino group from an amino acid to an								
CC	alpha-keto	acid using a claimed enzyme. The measurement of								
CC	aspartate	aminotransferase levels in blood serum is used as an								
CC	indicator	of heart damage.								
CC	Sequence	394 AA;								

		Query Match	10.7%	Score 402;	DB 26;	Length 394;
		Best Local Similarity	28.2%	Pred. No. 3,44e-21;		
		Matches	103;	Conservative	95;	Mismatches 139; Indels 28; Gaps 26;
Db	42	pfdftpdfkeaciralgktk-yapsagipelreaiaealklenkenveyk-pseiv-vs	98			
		:   :	:	: :	: :	:
QY	182	PAFTAVEADVAARVTGQFCNYCYPAGVGLPAAARSVAEHL-SQG-VPMILSADDVFUT	239			
		:   :	:	: :	: :	:
Db	99	agakmwllflfmailde-gdevlpspywvtypeqirffgvpv-evplkkekgfqsl	155			
		:   :	:	: :	: :	:
QY	240	AGGTQAI-EVIIIPVLAQTAGANTLLPRPCPNVEARAAP-NRLEVRHFDDLDPKGWEIDI	297			
		:   :	:	: :	: :	:
Db	156	edvkekvtter-thaivinspnntgtavveeeelkkiaefcver-gifilsdecyeyfyvg	213			
		:   :	:	: :	: :	:
QY	298	DSL-ESIAKNTTAMVIINPNPGSVGYDHLKSVAEY-AKRRLGITLVADEYQKLVLG	355			
		:   :	:	: :	: :	:



	DR	WPI; 96-518680/51.
	DP	N-PSDB; T38896.
	PT	Producing transgenic plants, with reduced climacteric ethylene prodn. - to give flowers and buds, specifically carnations, with increased post-harvest life
	PS	disclosure; page 40-42; 9ppp; English.
	CC	Carnation cv. White Sim i-aminocyclopentane-1-carboxylic acid (ACC) synthase (W04558) catalyses the initial step of ethylene biosynthesis in the plant. Its amino acid sequence was deduced from a full-length gene (T38896). Expression of a nucleic acid (T38897) coding for a fragment (W04559) of the ACC synthase in transgenic carnation reduces the formation of ACC synthase by co-suppression. The reduction in ACC synthase activity results in decreased climacteric ethylene prodn. by the plant and hence delayed senescence of flowers and buds after cutting, and increased post-harvest life.
	SQ	Sequence 517 AA;
		Query Match                  6.1%; Score 229; DB 20; Length 517; Best Local Similarity 27.1%; Pred. No. 7,24e+08; Matches 97; Conservative 91; Mismatches 139; Indels 31; Gaps
	Db	96 glpefrsavafmkardekvifnpdrvmvgasasetllfcfan-pgdaflipsyyp 150           :: : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	QY	211 GLPAARSVAHELSGGVPI-MLSADDDVFLTAGTOAIEVIPVLACTAGANILLPRPGYP 269       : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	Db	155 afndrlrwtgvnlipftccssnnfkitealqasyedalknikvkgilvtngsnplqt 210 ::: : : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	QY	270 NYEARAAFNRL-DEVHFDDLIPDKGEIDDSLESI-AD--KNTAM-VII-NPNPCGS 329 ::: : : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	Db	215 vldkdtlkmiltfnvaknhilvcdeiattvfnspsfiavaevikdmphvnqdvlhlyls 279           : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	QY	323 VYSYDHLKSVAEAKRGILVIADVEYVKLVGSAFFPMG-VF-G-HIIPVLS-IG-S 379           : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	Db	275 lskdmgpgvrfgviysyndr-vvstarmssf-g-l-vssq-tgfmaaalssdddfvrr 329           : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	QY	377 LSKSWIVPQWLGWAVYDPRKILOETFKISTITNVLNVSTDPATFIOALPLENTKE 439           : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	Db	330 -fivesrdrlfirhqhtselakig--igclq-gnaalfwmdlr-hlldeatverejkl 389           : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	QY	437 DFFKAIG-LUKESSEICYKOIKENKYITCPHPEGSFMVMKLNLHLEE--IDDDIDIF 499           : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	Db	385 wrviinekinvpsgsfscsepqfwrcfvamdnadtvalnrfsrtgrvdnst 442 ::: : : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	QY	494 CCKLAKESVILCPGSV-L-GMANVVRIIFACVP-SSLQDLGRKRKSCQRKNKNS 548 ::: : : : : : : :  ::  : : : :  ::  : : : :  ::  : : : :  ::
	RESULT	8
	ID	R89906 standard; Protein; 422 AA.
	DC	R89906;
	AT	15-JUL-1996 (first entry)
	DE	Human kynurenine aminotransferase (KAT).
	KW	Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;
	KX	kYN; brain; NMDA receptor; glutamateergic function.
	OS	Homo sapiens.
	PN	WO9601893-A1.
	PD	25-JAN-1996.
	PF	23-JUN-1995; UO7855.
	PP	07-JUL-1994; US-271667.
	PA	(PHAA ) PHARMACIA SPA.
	PA	(UYMA-) UNIV MARYLAND BALTIMORE.
	PI	Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;
	PI	Speciale C;
	DI	WPI; 96-097623/10.
	DR	N-PSDB; T11744.
	PT	Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) - useful in gene therapy applications and for identifying KAT in brain tissue
	PT	
	PS	Example 4; Figure 4; 51pp; English.
	CC	Sequences encoding Kynurenine aminotransferase (KAT) can be inserted into vectors and subsequently cells and hence can be used for gene therapy. The vector and host cells can be used for cerebral CC implantation to where KAT can directly catalyse the production of CC

	Query Match	5.58;	Score 207;	DB 17;	Length 423;
	Best Local Similarity	33.08;	Pred. No. 3.02e-06;		
	Matches 35;	Conservative 24;	Mismatches 46;	Indels 1;	Gaps 1;
Db	154	lgsasndwqlpaelaskftprtkvlnpnnplgkvsrmelvelvanicqhdvvcisd	213		
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
QY	287	LIPDKWEIDIDSGEADIADNTTAMTIIINPNCGSVSYVDHLKSKVAEAKRILGILVIAD	346		
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :			
Db	214	evqvgwlvdydghqnvstaslpqgmwdrlitigsagksfsatqkwqgv	259		

RESULT	11	
ID	R89998	standard; Protein; 457 AA.
AC	R89998;	
DT	14-JUL-1996	(first entry)
DE	Rat kynurenine aminotransferase (KAT) clone.	
DE	Kynurenine aminotransferase; KAT; kynurenic acid; KYNA; kynurenine;	
KW	KYN; brain; NMDA receptor; glutamatergic function.	
KW	Rattus rattus.	
OS	W09601893-A1.	
PN	25-JAN-1996.	
PD	23-JUN-1995; U07855.	
PF	07-JUL-1994; US-271667.	
PR	(PHAA ) PHARMACIA SPA.	
PA	(UYMA ) UNIV MARYLAND BALTIMORE.	
PI	Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;	
PI	Speciale C;	
DR	WPI; 96-097623/10.	
DR	N-PSDB: T11743.	

PT Isolated DNA encoding mammalian kynurenine amino-transferase (KAT) -  
 PT useful in gene therapy applications and for identifying KAT in brain  
 PT tissue  
 PS Claim 16; Figure 4; 51pp; English.  
 CC Sequences encoding kynurenine aminotransferase (KAT) can be inserted  
 CC into vectors and subsequently cells and hence can be used for gene  
 CC therapy. The vector and host cells can be used for cerebral  
 CC implantation to where KAT can directly catalyze the production of  
 CC kynurenine acid (KYNA) from kynurenine (KYN). It is thought KYNA acts  
 CC as a negative endogenous modulator of cerebral glutamatergic  
 CC function. KYNA concentrations and the activity of KAT show an  
 CC increase with age. KAT inhibitors, by providing an increase of the  
 CC glutamatergic tone at the NMDA receptor, could be useful in  
 CC situations where NMDA receptor function is insufficient and/or KAT  
 CC activity and KYNA levels are abnormally enhanced. Hence they could  
 CC be particularly useful in the treatment of the pathological  
 CC consequences associated with the aging processes in the brain.  
 CC Three KAT clones are described in T11560, T11742-43.  
 SQ Sequence 457 AA;

Query Match 5.5%; Score 207; DB 17; Length 457;  
 Best Local Similarity 33.0%; Pred. No. 3.02e-06;  
 Matches 35; Conservative 24; Mismatches 46; Indels 1; Gaps 1;  
 Db 188 lgsandwqlpaelskftprtkvlnvntpnplgkvfsmelvelvanlcqghdvcsid 247  
 QY 287 LIPDKGWEIDISLESIAKNTTAMVIINPNPCGVSVDHLSKVAEAKRLGILVIAD 346  
 Db 248 evyqvlvdyghvhsiaslpgmwdrtltigsagksfsatgkwgvw 293  
 QY 347 EYIGKLVLSGAPFIPMGVEGHI-TPVLSIGLSKSWIVPGWRLGW 391

RESULT 12  
 ID R25406 standard; Protein; 493 AA.  
 AC R25406;  
 DT 18-JAN-1993 (first entry)  
 DE ACC synthetase.  
 KW 1-aminocyclopropane-1-carboxylic acid synthetase; detriment;  
 KW ethylene; growth; maturity; aging; plant.  
 OS Cucurbita maxima.  
 PN J04169183-A.  
 PD 17-JUN-1992.  
 PF 31-OCT-1990; 296943.  
 PR 31-OCT-1990; JP-296943.  
 PA (SUMO) SUMITOMO CHEM CO LTD.  
 DR WPI: 92-253389/31.  
 DR N-PSDB; Q25896.  
 PT Detriment induced ACC synthetase gene - used for control of  
 PT bio-synthesis of ethylene, for controlling growth, maturity and  
 PT ageing of higher plant  
 PS Claim 2; Fig 1; 10pp; Japanese.  
 CC The protein sequence was deduced from the DNA sequence of the gene  
 CC encoding detriment induced 1-aminocyclopropane-1-carboxylic acid  
 CC (ACC) synthetase (EC 4.4.1.14) which was obtd. by screening a cDNA  
 CC library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtd. from  
 CC cDNA library clones was screened by an antibody method to identify  
 CC colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/PCMW33.  
 CC Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene  
 CC controls the growth, maturing and aging of higher plants.  
 SQ Sequence 493 AA;

Query Match 5.2%; Score 196; DB 5; Length 493;  
 Best Local Similarity 24.3%; Pred. No. 1.90e-05;  
 Matches 87; Conservative 101; Mismatches 140; Indels 30; Gaps 23;  
 Db 97 glpefrngiasfmgkvgvrgvafpsrvimgggatgasvtficlad-pgdaflypspy 155  
 QY 211 GLPAARSAVAEHLs--QGVFPYMLSDDDVLTAGTQAEIVIPVLAQTAGANILLPRGY 268  
 Db 156 aafdrldkwrtraqirvhnchsnfvtkaalelaykkaeanikvkgviitnpsnplg 215  
 QY 269 PNTEARAAP-NRLEVRHFDLIPDKGWEIDISLE-SI--A-DKNTAM-VII-NPNNPCG 321

Db 216 tttydrdtklvtvfnqndihldeiyatsvfkaptfisiagievehchckelihi 275  
 QY 322 SVYSDHLSKVAEAKRLGILVIADENVYKLVLSGAPIPMG--V--PGHITPVL-SIG- 375  
 Db 276 slskdmglpgfrvg-i-iysyndvv--vrrarqmssfglvssqtghllaamlsd--edfv 329  
 QY 376 SLRSKSWIPGVRGLGVAVYDPRKILQETKISTITNYLVNSTDPATFQAALPQILENTK 435  
 Db 330 dkflaenskraerharftkel-dkmgitclnsnag-vfvvmdlr-rlkqdtkaemel 386  
 QY 436 EDDFKAIITGLKESSEICYKOIKENKYITCPEKPEGSFVMVKLNLHL-EE-IDDIDF 493  
 Db 387 wrvinevklvpsgssfhvtepgwfrvcfanmddntvdvalnrhsvfvenidkkn 444  
 QY 494 CKLAKEESVILCPGSLGMAN--WWRITFACVP--SSLQDGLGRIKSPCQRKNRSS 548  
 RESULT 13  
 ID R08261 standard; protein; 175 AA.  
 AC R08261;  
 DT 18-FEB-1991 (first entry)  
 DE Peptide antigenic for malarial antiporozoite Antibodies.  
 KW Malaria; vaccine; universal carrier molecule.  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT duplication 1..160  
 FT /label= (-Asn-Ala-Ala-Gly-)3-40  
 FT duplication 161..175  
 FT /label= (-Lys-)1-15 (odd number)  
 FT cross\_links 161..175  
 FT /label= nth Lys has side chain identical to  
 FT AAs 1..n-1  
 PN EP-398443-A.  
 PD 22-NOV-1990.  
 PF 16-MAY-1990; 201244.  
 PR 19-MAY-1989; IT-020553.  
 PR 23-MAR-1990; IT-019800.  
 PA (ENIE) ENIERCERHE SPA.  
 PI Pessi A, Bonelli F, Chiappinelli L, Bianchi E, Del Giudice G;  
 DR WPI: 90-350221/47.  
 PT New immunogenic cpds. for synthetic vaccines for Plasmodium  
 PT malariae - and for determ. of antibodies of Plasmodium malariae  
 PS Claim 1; Page 15; 19pp; English.  
 CC Peptides have a fractal structure, branching at each lysine residue  
 CC into a side chain identical to all AAs at its N-terminal.  
 CC Peptides are useful as universal carrier molecules inducing  
 CC genetically unrestricted protective immunity against different  
 CC pathogenic agents.  
 CC Specifically, the peptides may be used as antigens in vaccination  
 CC and immunoassay of Plasmodium malariae antiporozoite antibodies.  
 CC See also R08260.  
 SQ Sequence 175 AA;

Query Match 5.0%; Score 186; DB 2; Length 175;  
 Best Local Similarity 32.0%; Pred. No. 9.99e-05;  
 Matches 40; Conservative 42; Mismatches 38; Indels 5; Gaps 5;  
 Db 2 aagnaagnaagnaagnaagnaagnaagnaagnaagna-gnaagna-naa-agnaagaa 59  
 QY 7 SDGVAANGLAVAAAANGKSNHGVA--VNGKSNHGVDADANGKSNHGVAADANGKSN 65  
 Db 60 gnaagnaagnaagnaagnaagnaagnaagnaagna-gnaagna-naa-gnaagna 118  
 QY 66 GHAEATANGHGEATANGKTNGHRESNGHAEAA--DANGESHAEDSANGESNGHAAAA 124  
 Db 119 agnaa 123  
 QY 125 EEEEA 129  
 RESULT 14  
 ID P90064 standard; protein; 429 AA.

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AC P90064;
DE 1-NOV-1989 (first entry)
DI Antigenic protein for malaria vaccination
KW Antigenic; vaccine; Plasmodium malariae;
KW circumsporozoite protein.
OS Plasmodium malariae
PN US7238746-A.
PD 16-MAY-1989.
PF 31-AUG-1988; 238746.
PR 31-AUG-1988; US-238746.
PA (USSH) Nat Inst of Health.
PI Lal A;
DR WPI: 89-172958/23.
PT Antigenic protein for vaccination against malaria
PT - encoded by cloned gene coding for Plasmodium
PT malariae circumsporozoite protein.
PS Disclosure; fig 1; lipp; English.
CC Antigenic circumsporozoite protein of Plasmodium malariae. Used
CC as a vaccine against malaria.
SQ Sequence 429 AA;

Query Match          5.0%; Score 189; DB 1; Length 429;
Best Local Similarity 28.0%; Pred. No. 6.08e-05;
Matches 45; Conservative 53; Mismatches 57; Indels 6; Gaps 6;

Db      Db      175 agnaagaaagnadgnaagaaagaaagaaagaaagaa-gnaagaaagaa-agnaagaaagaa 232
QY      QY      7 SDGVAANGLAFAAANKSGHGVAA--VNGKSNHGVDADANGKSNHGVAADANGKSN 65

Db      Db      233 gnaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa-gnaagaaagaa 291
QY      QY      66 GHAEATANGHEATANGKTNGHBESNGHAFAA-DANGESNEHAEDSAANGESNGHAAAA 124

Db      Db      292 agnaagaaagaaagaaagaaagneka-knkdknyvdantnkk 331
QY      QY      125 EEESEVWNNFAGKDGVLATGANMSIRAIRYKISASVQEK 165

RESULT 15
ID ID W21755 standard; Protein; 486 AA.
AC AC W21755;
DT DT 16-SEP-1997 (revised)
DT DT 26-AUG-1997 (first entry)
DE DE Poplar 1-aminocyclopropane-1-carboxylic acid synthase PNACC52.
KW KW Ozone; induction; exposure; resistance; transgenic plant; ACC;
KW KW 1-aminocyclopropane-1-carboxylic acid biosynthesis.
KW KW Populus nigra.
PN PN J09075088-A.
PD PD 25-MAR-1997.
PF PF 07-SEP-1995; 254510.
PR PR 07-SEP-1995; JP-234510.
PA PA (TOYT ) TOYOTA JIDOSHA KK.
PA WPI: 97-239270/22.
DR DR N-PSDB; T73502.
DR DR Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic
PT PT enzyme genes - from poplar tree, are useful for generating
PT ozone-resistant trees and pollution clean-up trees
PT Claim 2; Pages 9-11; 12pp; Japanese.
CS CS This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase
CC CC encoded by a cDNA clone isolated from poplar trees which
CC CC had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone
CC CC for 6 hours after one hour acclimation at 25 degrees C. 70 % relative
CC CC humidity, 30 k lux and air current 30 cm/second. The gene will be
CC CC useful for breeding air pollutant ozone-resistant trees, especially
CC CC poplar.
CC CC (Note: Record has been revised in order to correct the Organism
CC CC source field).
SQ SQ Sequence 486 AA;

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[illegible]

Search completed: Fri Oct 1 13:56:44 1999  
Job time : 41 secs.

QY	7	SDGVAAAGLVAATAAANGKSNHGHVAAA-VNGKSNHGHVADANGKSNHGCVAADANGKSN	65
Db	233	gnaagnaagnaagnaagnaagnaagnaagnaagnaagnaagnaagnaagnaagnaagna	291
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
QY	66	GHAETANGHEATANGKTNHRESNGHAPAA-DANGESNEHEDSAANGESNGHAAAA	124
Db	292	agnaagnaagnaagnaagnaagnekaknkdknvdatnkk	331
QY	125	EEEEAVENWFAGKDGVLAAATGANMSTRATRYKISASVOEK	165

RESULT	15	
ID	W21755	standard; Protein; 486 AA.
AC	W21755;	
DT	16-SEP-1997	(revised)
DT	26-AUG-1997	(first entry)
DE	Poplar 1-aminocyclopropane-1-carboxylic acid synthase PNACC2.	
DE	Ozone; induction; exposure; resistance; transgenic plant; ACC;	
KW	1-aminocyclopropane-1-carboxylic acid biosynthesis.	
KW	Populus nigra.	
OS	J09075088-A.	
PN	J09075088-A.	
PD	25-MAR-1997.	
PF	07-SEP-1995; 254510.	
PR	07-SEP-1995; JP-254510.	
PA	(TOYT ) TOYOTA JIDOSHA KK.	
DR	WPI: 97-239270/22.	
DR	N-PSDB; T73502.	
PT	Ozone-induced 1-amino-cyclopropane-1-carboxylic acid synthetic	
PT	enzyme genes - from poplar tree, are useful for generating	
PT	ozone-resistant trees and pollution clean-up trees	
PS	Claim 2; Pages 9-11; 12pp; Japanese.	
CC	This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase	
CC	encoded by a cDNA clone isolated from poplar trees which	
CC	had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone	
CC	for 6 hours after one hour acclimation at 25 degrees C, 70 % relative	
CC	humidity, 30 k lux and air current 30 cm/second. The gene will be	
CC	useful for breeding air pollutant ozone-resistant trees, especially	
CC	poplar.	
CC	(Note: Record has been revised in order to correct the Organism	
CC	Source field).	
CC	Sequence 486 AA;	
CC	Sequence 486 AA;	
CC	Sequence 486 AA;	

Query Match 5.0%; Score 185; DB 23; Length 486;  
Best Local Similarity 26.3%; Pred. NO. 9.99e-05;  
Matches 94; Conservative 89; Mismatches 144; Indels 30; Gaps 22;





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MAILED (TM)

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Fri Oct 1 13:55:14 1999; MasPar time 26.02 Seconds  
Tabular output not generated. 848.473 Million cell updates/sec

Title: >US-09-026-400-4  
Description: (1-551) from US09026400.peg  
Perfect score: 3749  
Sequence: 1 MATVRQSDGVAANGLAVAAA.....LGRIKFCQRNKKRNSSDDC 551

Scoring table: PAM 150  
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: pir60

1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 50.754; Variance 128.964; scale 0.394

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	952	25.4	454	1	tyrosine transaminase	1.52e-126
2	921	24.6	454	2	tyrosine transaminase	1.61e-121
3	489	13.0	429	2	probable aspc protein	7.03e-53
4	457	12.2	401	2	probable aspartate am	5.78e-48
5	402	10.7	394	2	aspartate aminotransf	1.30e-39
6	399	10.6	405	2	hypothetical protein	3.67e-39
7	374	10.0	402	2	aspartate transaminas	2.03e-35
8	370	9.9	375	2	aspartate transaminas	8.01e-35
9	359	9.6	397	2	hypothetical protein	3.44e-33
10	355	9.5	357	2	aspartate aminotransf	1.35e-32
11	353	9.4	390	2	hypothetical protein	2.66e-32
12	349	9.3	390	2	aspartate aminotransf	1.04e-31
13	344	9.2	392	2	aspartate transaminas	5.65e-31
14	323	8.6	379	2	aspartate aminotransf	6.71e-28
15	323	8.6	391	2	probable aspartate am	6.71e-28
16	319	8.5	393	2	aspartate aminotransf	2.56e-27
17	301	8.0	392	2	probable aspartate tr	1.03e-24
18	298	7.9	412	2	aspartate aminotransf	2.77e-24
19	294	7.8	374	2	aspartate aminotransf	1.04e-23
20	287	7.7	400	2	aspartate transaminas	1.04e-22
21	288	7.7	507	2	probable membrane pro	7.46e-23
22	289	7.7	592	2	probable membrane pro	5.37e-23
23	283	7.5	383	2	aspartate transaminas	3.84e-22

24	272	7.3	389	2	E71009	probable aspartate am	1.38e-20
25	274	7.3	432	2	F64484	alanine transaminase	7.23e-21
26	270	7.2	385	2	JC4537	aspartate transaminas	2.65e-20
27	271	7.2	390	2	F69452	aminotransferase (Asp	1.92e-20
28	259	6.8	373	2	E70338	aminotransferase (Asp	9.21e-19
29	255	6.8	389	2	S74343	aspartate aminotransf	3.32e-18
30	253	6.7	444	2	S56832	kynurenine aminotrans	6.29e-18
31	248	6.6	373	2	F69545	aspartate aminotransf	3.10e-17
32	248	6.6	389	2	S75949	hypothetical protein	3.10e-17
33	247	6.6	410	2	A40658	aspartate transaminas	4.26e-17
34	240	6.4	386	2	F64793	ybdL protein - Escher	3.90e-16
35	234	6.2	516	2	S19252	1-aminocyclopropane-1	2.58e-15
36	234	6.2	518	2	S31442	1-aminocyclopropane-1	2.58e-15
37	227	6.1	390	2	D70849	probable aminotransf	2.29e-14
38	230	6.1	401	2	S75385	probable aspartate tr	9.01e-15
39	230	6.1	482	2	S42535	alanine transaminase	9.01e-15
40	219	5.8	399	2	S39740	aspartate aminotransf	2.72e-13
41	218	5.8	482	2	S28429	alanine transaminase	3.72e-13
42	212	5.7	388	2	C70605	probable aminotransf	2.34e-12
43	212	5.7	412	2	H65011	hypothetical protein	2.34e-12
44	213	5.7	422	2	S52790	glutamine-phenylpyru	1.72e-12
45	214	5.7	465	2	H69777	transcription regulat	1.27e-12

#### ALIGNMENTS

RESULT 1

ENTRY XNRTY #type complete  
TITLE tyrosine transaminase (EC 2.6.1.5) - rat  
ALTERNATE\_NAMES tyrosine aminotransferase  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 26-Feb-1999  
ACCESSIONS A23310; A31804; JN0343; A48430; S18308; S17849  
REFERENCE A23310  
#authors Grange, T.; Guenet, C.; Dietrich, J.B.; Chasserot, S.; Fromont, M.; Belfort, N.; Jami, J.; Beck, G.; Pictet, R.  
#journal J. Mol. Biol. (1985) 184:347-350  
#title Complete complementary DNA of rat tyrosine aminotransferase messenger RNA. Deduction of the primary structure of the enzyme.  
#cross-references MUID:85293103  
#accession A23310  
#molecule\_type mRNA  
#residues 1-454 #label GRA  
#cross-references EMBL:X02741; NID:g57327; PID:g57328  
#note part of this sequence was confirmed by protein sequencing

REFERENCE A31804  
#authors Hargrove, J.L.; Scoble, H.A.; Mathews, W.R.; Baumstark, B.R.; Biemann, K.  
#journal J. Biol. Chem. (1989) 264:45-53  
#title The structure of tyrosine aminotransferase. Evidence for domains involved in catalysis and enzyme turnover.  
#cross-references MUID:89079691  
#accession A31804  
#molecule\_type mRNA  
#residues 226-284, 'G', 286-358, 'DL', 361-444, 'D', 446-454 #label HAR  
#note the authors translated the codon GGG for residue 285 as pro  
#note part of this sequence was confirmed by protein sequencing  
REFERENCE JN0343  
#authors Zelenin, S.M.; Popova, V.S.; Morozov, I.V.; Tishkav, V.I.; Egorov, A.M.; Mervetsov, N.P.  
#journal Bioorg. Khim. (1991) 17:994-996  
#title Nucleotide sequence of an EcoRI-fragment of the rat tyrosine aminotransferase gene determined on the automated sequencer "Applied Biosystems" model 370A.  
#cross-references MUID:92172066  
#accession JN0343  
#molecule\_type DNA

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##residues      385-454 ##label ZEL
##experimental_source liver
REFERENCE
#authors      Morozov, I.V.; Mishin, V.P.; Zelenin, S.M.; Popova, V.S.;
              Mertvetsov, N.P.
#journal      DNA Seq. (1990) 1:151-155
#title        Nucleotide sequence of rat liver tyrosine aminotransferase
              gene fragment.
#cross-references MUID:92190544
#accession     A48430
##status      preliminary
##molecule_type DNA
##residues     190-284,'L',286-386 ##label MOR
##cross-references GB:X15690; NID:g57845; PID:g1334238
##experimental_source liver
##note         sequence extracted from NCBI backbone (NCBIN:89708,
              NCBIP:89709)
REFERENCE
#authors      Lorber, B.; Dietrich, J.B.; Kern, D.
#journal      FEBS Lett. (1991) 291:345-349
#title        Isolation and characterization of active N-terminal truncated
              apo- and holoenzyme of mammalian liver tyrosine
              aminotransferase.
#cross-references MUID:92038067
#accession     S18308
##molecule_type protein
##residues     38-52;58-81 ##label LOR
##experimental_source liver
REFERENCE
#authors      Dietrich, J.B.; Lorber, B.; Kern, D.
#journal      Eur. J. Biochem. (1991) 201:399-407
#title        Expression of mammalian tyrosine aminotransferase in
              Saccharomyces cerevisiae and Escherichia coli. Purification
              to homogeneity and characterization of the enzyme
              overproduced in the bacteria.
#cross-references MUID:92037592
#accession     S17849
##status      not compared with conceptual translation
##molecule_type DNA
##residues     1,'V',3-10 ##label DIE
##experimental_source liver
GENETICS
#introns      408/3
CLASSIFICATION
#superfamily mammalian tyrosine aminotransferase
#acylated amino end: aminotransferase; homodimer;
#phosphoprotein; pyridoxal phosphate
FEATURE
383-394
1
#region PEST sequence\
#modified_site acetylated amino end (Met) #status
experimental\
#binding_site pyridoxal phosphate (Lys) (covalent)
#status experimental
SUMMARY
#length 454 #molecular-weight 50635 #checksum 7044
Query Match      25.4%; Score 952; DB 1; Length 454;
Best Local Similarity 34.8%; Pred. No. 1.52e-126;
Matches 139; Conservative 120; Mismatches 130; Indels 11; Gaps 10;
Db      49 SNKTFNPIRAIVDMKVPNPKTVISLSIGDPTVFGNLPDPTVQAMKDALDSGKYNG 108
QY      147 ANMSIRAIRYKISA-SVOEKGPRVLPVLAHGDSPVFAFTAVEADAFAAATVGTGFNC 205
Db      109 YAPSIGVLSRSEVASYHCHCAP--LEAKDVILTSCSOAIECLAVLAN-PQONILIP 165
QY      206 YPAGVGLPAARSVAEHL-SQGVPMYLSADDVFLTAGTQAEIVLPVLAQTAGANILLP 264
Db      166 RPFSLVRYTIAESMGIEVKYNLLPERSWEIDLKQLESIDIEKTAFLVNNPNSPCGSVF 225
QY      265 RPYGVNPEARAAFNRLVRFHFDLPDKRGWEIDLSLESIADKNNTAMVIINPNPCGSVY 324
Db      226 SKRHLOKTLVAERQCVPILADEITYGDMVFSDCKEYEPLANLSTNVPILSCGGIAKRWLP 285
QY      325_SYDHLKVAEAKRGLIVIADEYIGKLVLSGSAFFIPMGVFGHTTPVLISLGSLSKSWIVP 384

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Db      286 GWRLGWLIIHRRDIF-GNEIRDGLVKLSORILGPTCTIVOGALKSILQRTPOEFYHDTLS 344
QY      385 GWRLGWAIVYDPKILQETKISTITNYLNWSTDPATFIOAALPQILENTKEDFFKAIG 444
Db      345 FLKSADNLGALAAIPGLQ-EVRFSGAMLYMGVEMEHFPEFENDVEFERLIAEQAV- 402
QY      445 LLKESSEICYKIKENKYITCPHKPEGSMFVAVKLNHLLEIDDDIDDCCKLAKEESVI 504
Db      403 HCLPATCFEYPNFFRVVIT-VPEVMVMLEACSRIOEQECQH 441
QY      505 LC-PGSVLGMANWVRITFACVPSSLQ-DGLGRIKSFQCRN 542
RESULT      2
ENTRY
TITLE      tyrosine transaminase (EC 2.6.1.5) - human
ALTERNATE_NAMES
ORGANISM   rat; tyrosine aminotransferase
ORGANISM   #formal_name Homo sapiens #common_name man
DATE      04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change
ACCESSIONS
REFERENCE   S10887
#authors    Rettenmeier, R.; Matt, E.; Zentgraf, H.; Scherer, G.
#journal    Nucleic Acids Res. (1990) 18:3853-3861
#title      Isolation and characterization of the human tyrosine
              aminotransferase gene.
#cross-references MUID:90326506
#accession  S10887
##molecule_type DNA
##residues   1-454 ##label RET
##cross-references EMBL:X52509; NID:g36696; PID:e225804; PID:g1217965
REFERENCE   S21425
#authors    Seraini, G.E.; Breton, N.; Berube, D.; Gagne, R.; Labrie, F.
#submission submitted to the EMBL data library, September 1990
#description Nucleotide sequence of human tyrosine aminotransferase
              cDNA.
#accession  S21425
##molecule_type mRNA
##residues   1-454 ##label SER
##cross-references EMBL:X55675; NID:g37501; PID:g37502
REFERENCE   S52087
#authors    Seraini, G.E.; Luu-The, V.; Labrie, F.
#journal    Biochim. Biophys. Acta (1995) 1260:97-101
#title      Cloning and expression of human tyrosine aminotransferase
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#cross-references MUID:95092801
#accession  S52087
##status     preliminary
##molecule_type mRNA
##residues   1-454 ##label SE2
##cross-references EMBL:X55675; NID:g37501; PID:g37502
REFERENCE   S60718
#authors    Zelenin, S.M.; Mertvetsov, N.P.
#journal    Bioorg. Khim. (1994) 20:196-204
#title      Nucleotide sequence of human tyrosine aminotransferase
              gene.
#accession  S60718
##molecule_type DNA
##residues   1-454 ##label ZEL
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#gene       GDB:TAT
##cross-references GDB:120398; OMIM:276600
#map_position 16q22.1-16q22.3
#introns    79/1; 114/1; 136/3; 189/3; 236/1; 253/3; 304/3; 347/3; 375/3;
              408/3
CLASSIFICATION
#superfamily mammalian tyrosine aminotransferase
#aminotransferase
#length 454 #molecular-weight 50399 #checksum 6711
KEYWORDS
Query Match      24.6%; Score 921; DB 2; Length 454;
Best Local Similarity 33.3%; Pred. No. 1.61e-121;
Matches 133; Conservative 123; Mismatches 134; Indels 9; Gaps 9;
Db      49 AKTTFNPIRAIVDMKVPNPKTVISLSIGDPTVFGNLPDPTVQAMKDALDSGKYNG 108

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QY	211	GLPAARSAAEH-LSQGVPMYLSADDFVLTAGGTQAIEVPIVLAQTAGANILLPRGYP	269
Db	156	LWTASTSLAGTGPVHY-LCDETQGWQDPIADLESKITER-TKALVINPNPNTGAVTSC	213
QY	270	NYEAAAFNRLEVRHFDLIPDK-GWEIDDSLES-IAKNNTAMVINPNPCGVSIVSYD	327
Db	214	ILTQWDLARKHQLLADDEIYDKILYDDAKHISLASIADPMCLCTNGLSKAYRVAGYR	273
QY	328	HLSKVAEVARGLTIVADEVYKGLVLSGAPFIPMGVFGHITPTVLSLGSLSKSWIVPCWR	387
Db	274	AGWLAIITGPREHASSFTIEGTLNMLRCPNVPQAHAIQVALGG-HQSI-EDLVLPQGR	331
QY	388	LGVAVYDPRKIILOETKISTITNVLNSYD-PATF-IOAALPOILENTDFEKKAIIGL	445
Db	332	L-EORDIAWTKLNEIPGVSCV-KPAGALYAFPRLDPEYD-IDDDEQLVLDLLSEKILV	388
QY	446	LKESSEICYQIKENKVIITCPHRPEGSFMVVKLNLLHLEIDDDIDDFCCLAKESVIL	505
Db	389	TQGT 392	
QY	506	CPGS 509	
RESULT	4		
ENTRY	D71003	#type complete	
TITLE	probable aspartate aminotransferase - Pyrococcus horikoshii		
ORGANISM	#formal_name Pyrococcus horikoshii		
DATE	14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change		
ACCESSIONS	D71003		
REFERENCE	A71000		
#authors	Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.; Hoshoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.; Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.; Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.		
#journal	DNA Res. (1998) 5:55-76		
#title	Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3.		
#cross-references	MUID:98344137		
#accession	D71003		
#status	preliminary; nucleic acid sequence not shown; translation not shown		
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#experimental_source	strain OT3		
#note	this accession replaces an interim accession for a sequence replaced by GenBank		
GENETICS			
#gene	PH1322		
SUMMARY	#length 401 #molecular-weight 45564 #checksum 5232		
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Best Local Similarity	29.0%; Pred. No. 5.78e-48;		
Matches	93; Conservative 83; Mismatches 132; Indels 13; Gaps 12;		
Db	28	LEKKGK-VIRLNTIGDPVKF-DFQPPHMKRAYCRAIQEGH-NYIGDSEGLIELREAIK	84
QY	162	VOEKGPRVPLAHGDDSVPAFTAVEAEAAVAVRTGQFNCYPAGVGLPAARSAVAE	221
Db	85	REKEKNGVDITPDVRYTAAVTEALQILFGALLD-PGEILIPGSPYPTGLVKFYGGK	143
QY	222	HLSQGVPMYLSADDFVLTAGGTQAIEVPIVLAQTAGANILLPRPGYPNTEAARFNRLE	281
Db	144	PVEYRTIEESGWQPDIDRLKTSER-TKAIIVINPNPCTALYDKKTIIEIINVAGEHD	202
QY	282	VRHFDLPDKGWEIDDSL-ESTADIKNTTAMVINPNPCGVSIVSYDHLKVAEVARKL	340
Db	203	LVLISDEIYDLMTYEGRHISP-GSLTKDVPVIVNGLSKYVFATGWRILGYMYFVDPBGL	261

Qy	341	ILVTADEVYGLVGSAPFIPMGVFGHTVPLSTGSLKSNVPGWRLGWVAYDPRKIL	400
Db	262	SEVREADIKLARICPNTPCQF--AAIAG-LTGSMDYLKMKYMKLKRDRDIYKRLNE	317
Qy	401	QETKISTISINLVNSTD-PATFIOALPOLLENTREDFKAIIGLLKESSEICYQIKRE	459
Db	318	IPGIS-TTKPGOGAFYIPPRIE	337
Qy	460	NKYITCPHKPEGSMFVMVKLN	480
RESULT	5		
ENTRY	A70469	#type complete	
TITLE	aspartate aminotransferase - Aquifex aeolicus		
ORGANISM	#formal_name Aquifex aeolicus		
DATE	08-May-1998	#sequence_revision 08-May-1998	#text_change 13-Sep-1998
ACCESSIONS	A70469		
REFERENCE	A70300		
#authors	Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Sneed, M.A.; Keller, M.; Aulaj, M.; Huber, R.; Feldman, R.A.; Short, J.M.; Olson, G.J.; Swanson, R.V.		
#journal	Nature (1998) 392:353-358		
#title	The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.		
#cross-references	Mttd:98196666		
#accession	A70469		
#status	preliminary; nucleic acid sequence not shown; translation not shown		
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#residues	1-394	#label AOF	
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GENETICS			
#gene	aspC1		
CLASSIFICATION	superfamily aspartate transaminase		
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Best Local Similarity	28.2%; Pred. No. 1.30e-39;		
Matches	103; Conservative 95; Mismatches 139; Indels 28; Gaps 26;		
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Db	99	AGAKWLFILMAILDE-GDEVLLSPSYWVTPQIRFFGGVPV-EVPLKKEGQOLS	155
Qy	240	AGGTQAI-EVIIPVLAOTAGANILLPRPGPNYEAAAF-NRLEVRHFDLPDQGEIDI	297
Db	156	EDVKEKTER-TRAVILSNPNPTGAVYEELKKAFCVER-GIFILSDECYEYFVVG	213
Qy	298	DSL-ESTADNTMTAVLINPNPCGSYVDHLSKVAEV-AKRLGILVIADEVIGKLVLG	355
Db	214	DAKEVSPASDESCKNTITFTVNAFSSYSMTGRIGYVA-C-P-E-EYAKVIASLNS-Q	267
Qy	356	SAPFIPMGVFGH-ITPV-LSIGLSKSWIPGWRGLGWAVYDPRKILQETKISTISNYL	413
Db	268	SVS-NVITFAQYAGAL-PALKNPYSKDFVNMENRANAFERRDTAVEELSKIPGMDV-V	324
Qy	414	NVSDPATFIO-AALPOILENTKE-DFFKAIIGLLKESSEICYQIKENKYYITCPHKPEG	471
Db	325	AFYTFPDSAYA-EKLGDDVKLSEFLLEKAVVPGPSAFGPFGLRLSYALSEERLVEG	383
Qy	472	SMFVMVKLNHLLEEIDDDIDFCKLAKESVILCPGSLGMANWRIITFACVPSSLQDG	531
Db	384	IRRIK	388
Qy	532	LGRIK	536

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TITLE       hypothetical protein b2290 - Escherichia coli (strain K-12)
ORGANISM    #formal_name Escherichia coli
DATE        12-Sep-1997   #sequence_revision 17-Sep-1997   #text_change
                        14-Nov-1997
ACCESSIONS  H65000
REFERENCE   A64720
#authors    Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
            Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
            Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
            Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao
            Y.
#journal     Science (1997) 277:1453-1462
#title       The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession  H65000
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            UNGP:b2290
##experimental_source strain K-12, substrain MG1655
SUMMARY      #length 405 #molecular_weight 45517 #checksum 4760

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Matches 96; Conservative 99; Mismatches 154; Indels 16; Gaps 16;

Db 17 IRGVLKEAKRLKEEGNK-VLKLNIGNPAPP-GFDAPDEILVDVIRNLPTAQ-G-YCDSK 72
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Qy 151 IRAIRYKISASVOEKGRPVPLAHGDPSVFPAFRTAVEADAAVAARTGFNCYPAGV 210
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :

Db 73 GLYSARKAIMQHQAQRMDV-TVEDIYTGVSESLIVQMAGALLNS-GDEMVLVPADPY 130
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Qy 211 GLPAARGAFAEHL-SOGVPYMLSDADVFTTAGGTQAEIVIPVLAQTAGANTILLPRPGVP 269
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Db 131 LWTAAVLSLSSGKAHVH-LCDESDDWPFDDDIRAKITPTRGTVIINPNNPYGAVYSKEL 189
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Qy 329 LSKVAEYAKRLGLIVIADEVYGLVLGSAPFIPMGVFGHTTPVLSTIGSLSKSWIPVGWRL 388
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Db 250 GWMYLVNPKKHAKGYIEGLEMASMRCLCANVPAQHAIQIALGY-QSISE-FITPG-GRL 306
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Db 307 YEQRNRRAWELNDIPGVSCV-KPRGALYMFEPKIDAKRFN-IHDDQKWLDLLEQKVLLV 364
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Qy 447 KESSEICYKQLKENKYITCPHKPEGSVMVVKULNHLLHEIDDIDDFCKCLAKEESVILC 506
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Db 365 QGTAF 369
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Qy 507 PGSVL 511

RESULT      7
ENTRY       S07088          #type complete
TITLE       aspartate transaminase (EC 2.6.1.1) - Sulfolobus solfataricus
ALTERNATE_NAMES aspartate aminotransferase
ORGANISM    #formal_name Sulfolobus solfataricus
DATE        29-Jan-1993   #sequence_revision 29-Jan-1993   #text_change
                        13-Sep-1998
ACCESSIONS  S07088; S27106; S45613
REFERENCE   S07088
#authors    Cubellis, M.V.; Rozzo, C.; Nitti, G.; Arnone, M.I.; Marino,
            G.; Sannia, G.
#journal     Eur. J. Biochem. (1989) 186:375-381
#title       Cloning and sequencing of the gene coding for aspartate
            aminotransferase from the thermocacidophilic archaeobacterium

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#journal	#title
Eur. J. Biochem. (1989) 186:375-381	Cloning and sequencing of the gene coding for aspartate aminotransferase from the thermoacidophilic archaeobacterium

**#authors**  
Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; Fitzgerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagsels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;

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Matches 93; Conservative 86; Mismatches 163; Indels 19; Gaps 17;

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Db 99 AKQSLFNAIQALIE-EGDDEVIIPVFWTYPELVKYSQ-GVSQFQTQDSEKSHFTPKQL 156
QY 242 GTQAEVIVPVLQAQTAGANILLPRGYPNYEARAFNRLEVRHFDLIPDKG-WEIDIDSL 300
Db 157 KDALSPK-TKMLILTPSNPTGMLYSKAELEALGEVLKDKTKYMWLSDEIYEKLVY-KGEF 214
QY 301 -ESIADKNTTAMVIINPNPCGVSVDHLSKVAEVAERGLGILVIADEYVGLVLSGAPF 359
Db 215 VSCAAVSEMKRRTITIGLSKSVAMTGWRMGYAASKOKKLVKLMNLSQOCTSNISIT 274
QY 360 IP-MGVFGHIT-PVLSIGLSKSVIWPGRWLGVAVIDPRKILQETKISTITNVLNST 417
Db 275 QMAS-I-VAL-EGLYD-KE--IETMRQAFERCDLAHAKINAIGLN-ALKPDGAFYLF 327
QY 418 DPATFIQAALPOLIENTREDFKAIIGLLKESSEICYQIKENKYYITCPHKPEGSFVNV 477
Db 328 HTG-SLCG--GDSMRFCHELLEKEGVALVPGKAFGLEGVYVLSFACSEEQIEKGIERIAR 384
QY 478 KLNHLLEEIDDDIDFCCKLAKEESVILCPGSLGMANNWVRITFACVPSSLDGLGRIS 537
Db 385 F 385
QY 538 F 538

RESULT 12
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TITLE   aspartate aminotransferase - Helicobacter pylori (strain J99)
ORGANISM #formal_name Helicobacter pylori
VARIETY  strain J99
DATE    12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change
        05-Mar-1999
ACCESSIONS H71909
REFERENCE  A71800
AUTHORS   Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.;
           Doig, P.C.; Smith, D.R.; Noonan, B.; Guild, B.C.; deTonge,
           B.L.; Carmel, G.; Tummino, P.J.; Caruso, A.;
           Uria-Nickelsen, M.; Mills, D.M.; Ives, C.; Gibson, R.;
           Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis,
           G.F.; Trust, T.J.
JOURNAL   Nature (1999) 397:176-180
TITLE     Genomic sequence comparison of two unrelated isolates of the
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CROSS-REFERENCES MUID:99120557
ACCESSION H71909
STATUS    preliminary
MOLECULE_TYPE DNA
RESIDUES  1-390 #label ARN
CROSS-REFERENCES GB:AE001493; GB:AE001439; NID:g4155161; PID:g4155168
EXPERIMENTAL_SOURCE strain J99

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SUPERFAMILY aspartate transaminase
CLASSIFICATION #length 390 #molecular-weight 42746 #checksum 4845
SUMMARY

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Db 40 PDFTPQAIKDAAIKALNDG-FTKYPVAGIPPELLKAIKAFKLNKNNLDYEPSEILVNSG 98
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Db 157 KDALSPK-TKMLILTPSNPTGMLYSKAELEALGEVLKDKTKYMWLSDEIYEKLVY-KGEF 214
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QY 418 DPATFIQAALPOLIENTREDFKAIIGLLKESSEICYQIKENKYYITCPHKPEGSFVNV 477
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Db 385 F 385
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ORGANISM        #formal_name Bacillus sp.
DATE            23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
        13-Sep-1998
ACCESSIONS A38621
REFERENCE  A38621
AUTHORS   Sung, M.H.; Tanizawa, K.; Tanaka, H.; Kuramitsu, S.;
           Kagamiyama, H.; Hirotsu, K.; Okamoto, A.; Higuchi, T.;
           Soda, K.
JOURNAL   J. Biol. Chem. (1991) 266:2567-2572
TITLE     Thermostable aspartate aminotransferase from a thermophilic
           Bacillus species. Gene cloning, sequence determination, and
           preliminary X-ray characterization.
CROSS-REFERENCES MUID:91115885
ACCESSION A38621
STATUS    preliminary
MOLECULE_TYPE DNA
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CROSS-REFERENCES GB:M59430; NID:g142537; PID:g142538
KEYWORDS  #superfamily aspartate transaminase
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QY 182 PAFTAVEAEDAFAAARTGQFNCYPAGVGLPAARSAVAEHLSSQGVPMYLSADDVFLTAG 241
Db 101 AKHVLTYLTFQVILN-EGDEVIIPIYVWYTPQYKLAG-GVPVYIATSEQNYKITABQL 158
QY 242 GTQAEVIVPVLQAQTAGANILLPRGYPNYEARAFNRLEVRHF-DLIPDKGWEIDIDSL 300
Db 159 KNAITDK-TRAVIINSNPTGMVYTRREEEDIAKIALENNILIVSDEIYEKLYNGAEH 217
QY 301 -ESIADKNTTAMVIINPNPCGVSVDHLSKVAEVAERGLGILVIADEYVGLVLSGAPF 358

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Db	329	DVS-EAAQKTGFASVDEFASALLTEANVAVIPGSGFGAPSTIRISYATSLNLEAEIRI	387
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ORGANISM		#formal_name Archaeoglobus fulgidus	
DATE		05-Dec-1997	#sequence_revision 05-Dec-1997
		13-Sep-1998	#text_change
ACCESSIONS		A69516	
REFERENCE		A69250	
Authors		Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kervavage, A.R.; Graham, D.E.; Kyripides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Doughterty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.	
#journal		Nature (1997) 390:364-370	
#title		The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Archaeoglobus fulgidus.	
#cross-references		MUID:98049343	
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Db	101	AKYAIFAMCCLL-OEGDEVILLD-PSWSYEA-CIL-MAGAKPVWVPEHEGE-D-API	154
QY	242	GTQAI-EVILPVAQTAGANILLPRGYPNYEARAAFNLEVRHFDLPDKGWEIDIDSL	300
Db	155	EDYITSNTKMLVNTPSNLGVWPKFELKVRDLADVDRKILVMSDEIYEKIFEGEHS	214
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Fri Oct 1 16:47:09 1999

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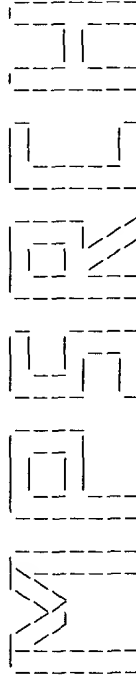
Page 9

QY 533 GRI 535

Search completed: Fri Oct 1 13:55:46 1999  
Job time : 32 secs.



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\*\*\*\*\* (TM) \*\*\*\*\*

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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:53:33 1999; MasPar time 17.07 Seconds  
 912.281 Million cell updates/sec  
 Tabular output not generated.

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 Perfect Score: 3749  
 Sequence: 1 MATYRQSDGVAANGLAVAAA.....LGRKSFQCRNKRNSDDC 551

Scoring table: PAM 150  
 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot37  
 1:swissprot

Statistics: Mean 51.972; Variance 111.846; scale 0.465

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

# SUMMARIES

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2	921	24.6	454	1	ATTY_HUMAN	2.25e-143
3	586	15.6	416	1	ATTY_TRYCR	2.66e-80
4	374	10.0	401	1	AAT_SULSO	5.21e-42
5	370	9.9	375	1	AAT1_METJA	2.61e-41
6	344	9.2	392	1	AAT1_BACSF	8.63e-37
7	336	9.0	393	1	AAT1_BACSU	2.07e-35
8	319	8.5	393	1	PATA_BACSU	1.69e-32
9	304	8.1	392	1	PATA_BACSU	5.95e-30
10	287	7.7	400	1	AATA_RHME	4.29e-27
11	288	7.7	507	1	ALAT_YEAST	2.92e-27
12	289	7.7	592	1	ALAM_YEAST	1.98e-27
13	253	6.7	444	1	YUGO_YEAST	1.73e-21
14	251	6.7	505	1	ALAT_SCHPO	3.65e-21
15	247	6.6	421	1	AATB_RHME	1.62e-20
16	244	6.5	410	1	YDT4_SCHPO	4.94e-20
17	240	6.4	386	1	YBDL_ECOLI	2.17e-19
18	230	6.1	482	1	ALAD2_HORVU	8.54e-18
19	229	6.1	517	1	1A1C_DIACA	1.23e-17
20	219	5.8	399	1	AAT2_BACSU	4.62e-16
21	218	5.8	482	1	ALAD2_PANMI	6.62e-16
22	212	5.7	412	1	YFDZ_ECOLI	5.68e-15
23	202	5.4	213	1	AAT_STRGR	1.97e-13

24	202	5.4	387	1	PATB_BACSU	PUTATIVE AMINOTRANSFER	1.97e-13
25	194	5.2	418	1	YD91_METJA	PUTATIVE AMINOTRANSFER	3.22e-12
26	196	5.2	493	1	1A11_CUCMA	1-AMINOCYCLOPROPANE-1-	1.60e-12
27	193	5.1	361	1	HIS8_HALVO	HISTIDINOL-PHOSPHATE A	4.55e-12
28	190	5.1	393	1	CSP_PLABR	CIRCUMSPOROZOITE PROTE	1.28e-11
29	182	5.1	475	1	1A12_CUCMA	1-AMINOCYCLOPROPANE-1-	6.43e-12
30	188	5.0	429	1	CSP_PLAMA	CIRCUMSPOROZOITE PROTE	2.55e-11
31	187	5.0	495	1	ALAT_RAT	ALANINE AMINOTRANSFERA	3.60e-11
32	184	4.9	347	1	MSA2_PLAF2	MEROZOITE SURFACE ANTI	1.00e-10
33	184	4.9	385	1	HIS8_YEAST	HISTIDINOL-PHOSPHATE A	1.00e-10
34	183	4.9	419	1	CSP_PLACC	CIRCUMSPOROZOITE PROTE	1.41e-10
35	185	4.9	493	1	1A11_CUCPE	1-AMINOCYCLOPROPANE-1-	7.13e-11
36	180	4.8	390	1	MALY_ECOLI	MALY PROTEIN (EC 2.6.1	3.90e-10
37	181	4.8	470	1	YJIR_ECOLI	HYPOTHETICAL 53.0 KD P	2.78e-10
38	178	4.7	376	1	HIS8_SULSO	HISTIDINOL-PHOSPHATE A	7.65e-10
39	177	4.7	494	1	1A12_CUCPE	1-AMINOCYCLOPROPANE-1-	1.07e-09
40	174	4.6	219	1	HIS8_MYCM	HISTIDINOL-PHOSPHATE A	2.93e-09
41	174	4.6	398	1	CSP_PLACC	CIRCUMSPOROZOITE PROTE	2.93e-09
42	174	4.6	476	1	1A14_LYCFS	1-AMINOCYCLOPROPANE-1-	2.93e-09
43	172	4.6	495	1	ALAT_HUMAN	ALANINE AMINOTRANSFERA	5.70e-09
44	168	4.5	401	1	CSP_PLACC	CIRCUMSPOROZOITE PROTE	2.14e-08
45	165	4.4	384	1	HIS8_SCHPO	HISTIDINOL-PHOSPHATE A	5.72e-08

## ALIGNMENTS

RESULT 1  
 ID ATTY\_RAT STANDARD; PRT; 454 AA.  
 AC P04694;  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE  
 DE AMINOTRANSFERASE) (TAT).  
 GN TAT.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;  
 OC RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 85293103.  
 RA GRANGE T., GUNET C., DIETRICH J.-B., CHASSEROT S., FROMONT M.,  
 RA BEFORT N., JAMI J., BECK G., PICTET R.;  
 RT "Complete complementary DNA of rat tyrosine aminotransferase  
 RT messenger RNA. Deduction of the primary structure of the enzyme.";  
 RL J. MOL. BIOL. 184:347-350(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE; 89079691.  
 RA HARGROVE J.L., SCOBLE H.A., MATHEWS W.R., BAUMSTARK B.R.,  
 RA BIEMANN K.;  
 RT "The structure of tyrosine aminotransferase. Evidence for domains  
 RT involved in catalysis and enzyme turnover.";  
 RL J. BIOL. CHEM. 264:45-53(1989).  
 RN [3]  
 RP SEQUENCE OF 190-386 FROM N.A.  
 RC TISSUE=LIVER;  
 RX MEDLINE; 92190544.  
 RA MOROZOV I.V.;  
 RT "Nucleotide sequence of rat liver tyrosine aminotransferase gene  
 RT fragment.";  
 RL DNA SEQ. 1:151-155(1990).  
 RN [4]  
 RP PARTIAL SEQUENCE.  
 RX MEDLINE; 92038067.  
 RA LORBER B., DIETRICH J.-B., KERN D.;  
 RT "Isolation and characterization of active N-terminal truncated apo-  
 RT and holoenzyme of mammalian liver tyrosine aminotransferase.";  
 RL FEBS LETT. 291:345-349(1991).  
 RN [5]  
 RP STRUCTURAL PROPERTIES.  
 RX MEDLINE; 89000971.  
 RA DIETRICH J.-B., GENOT G., BECK G.;

RESULT	2	
ID	ATTY HUMAN	STANDARD; PRT; 454 AA.

[illegible]



```
QY 242 GTOAIEVPIPVLAQTAGANILLPRGYPNYEARAFNRLEVRHFDLIPDKGWEIDIDSL- 300
Db 149 ESIT-KTKLIIFSPNPTGKVVYDKETIKGLAEIAEDYNLIIVSDVYDKKIYDKKHY 207
QY 301 ESIADKNTAMVINPNPCGSVSYDHLKVAEAKRGLIVIADEVYKVLVSAPFI 360
Db 208 PMQ-FTD-RCIL-INGFSKTYAMTGWIRIGYLAVSDELKELDLINMIKIHOY-SFAC-A 262
QY 361 PMGVEGHTPVLSTGSLSKSWIVPGWRLGWAVYDP-RKILQETKISTITNLYNVSTDP 419
Db 263 TTEAQYGALAA-LRGS-QKCVEDMVRFKMRDLINGLKD-I-FKV--NKPDGA-FY-I- 314
QY 420 ATFIQ-AALPOLIENTEDFFKALIGLKSSEICYKQIKENYITCPCPKPGSMFVWK 478
Db 315 FP-DV-SEYGVGEVAKKLI-ENKV-LCVPGVAFGNGANGYIRFSYATRYEDIERKALGII 370
QY 479 LNLHLEEDIDDFCKLAKESVILC-PGSVLG-M-ANWVRITFACVPSSLQDGLGRI 535
Db 371 K 371
QY 536 K 536

RESULT 6
ID AAT_BACSP STANDARD; PRT; 392 AA.
AC 223034; 1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 34, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSMINASE A) (ASPART).
OS BACILLUS SP. (STRAIN YN-2).
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91115885.
RA HIROTSU K., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
RA SUGA K., OKAMOTO A., HIGUCHI T., SODA K.;
RT "Thermostable aspartate aminotransferase from a thermophilic Bacillus
RT species. Gene cloning, sequence determination, and preliminary X-ray
RT characterization.";
RJ J. BIOL. CHEM. 266:2567-2572(1991).
RN [2]
RP SEQUENCE OF 1-24 AND 387-392.
RX MEDLINE; 90170846.
RA SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
RA SODA K.;
RT "Purification and characterization of thermostable aspartate
RT aminotransferase from a thermophilic Bacillus species.";
RJ J. BACTERIOL. 172:1345-1351(1990).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- THIS THERMOSTABLE ENZYME IS MOST ACTIVE AT 70 DEGREES CELSIUS.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL; M59430; G142538; ..
CC PIR; A38621; A38621
CC PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
CC PFAM; PF00155; aminotran_1; 1.
KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT CONFLICT 388 388 D -> L (IN REF. 2).

SQ SEQUENCE 392 AA; 42661 MW; 8FOEC6D0 CRC32;
Query Match 9.2%; Score 344; DB 1; Length 392;
Best Local Similarity 23.7%; Pred. No. 8.63e-37;
Matches 86; Conservative 103; Mismatches 154; Indels 20; Gaps 18;

Db 42 PDNTONIMDAIDSMMQOG-YTKYTPSGGLPALKQAIIEKFRDNQLEYKPNIEIVGV 100
QY 182 PAFRTAVEADEAFAVARTQCFNCYPAAGVGLPAARSVAEHLSCQVYMLSADDVFLTAG 241
Db 101 AKHVLATLFOVLN-BGDEVILPIPVWVSYPQVQVLAG-GVPVYIETATSEQNYKITAOL 158
QY 242 GTOAIEVPIPVLAQTAGANILLPRGYPNYEARAFNRLEVRHFDLIPDKGWEIDIDSL 300
Db 159 KNAITDK-TKAVIINSNPTGMVYTRREELEDAKALENNILIVSDIYIEKLYNGAEH 217
QY 301 -ESIAKNTTAMVINPNPCGSVSYDHLKVAEAKRGLIVIADEVYKVLV-GSAP 358
Db 218 FSTAQISEEVKAQTIINGVSKSHSMTGHRIGYAG-NADIINAMTDLASHSTSNPTTAS 276
QY 359 FIPMGVEGHI-TPVLSIGLSKSWIVPGWRLGWAVYDPKILQETKISTITNLYNVST 417
Db 277 QYAAIEAYNGPQ--DSV-BEMRKAFESRL-ET--I-YPKLSAIPGFKVY-KPGAFYLLP 328
QY 418 DPATFIOAALPOLIENTEDFFKALIGLKSSEICYKQIKENYITCPCPKPGSMFVWK 477
Db 329 DVS-EAAQKTGFASVDFASALLTEANVAVIPGSGFAPSTIRISYATSLNIEAERI 387
QY 478 KNLHLEEDID-DFCKLAKESVILC-PGSVLG-MANWVRITFACVPSSLQDGLGRI 535
Db 388 DRF 390
QY 536 KSP 538

RESULT 7
ID AAT_BACST STANDARD; PRT; 393 AA.
AC Q59228;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSMINASE A) (ASPART).
GN ASPC.
OS BACILLUS STEAROTHERMOPHILUS.
OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC BACILLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-ATCC 12980;
RX MEDLINE; 96434469.
RA BARTSCH K., SCHNEIDER R., SCHULZ A.;
RT "Stereospecific production of the herbicide phosphinothricin
RT (glufosinate): purification of aspartate transaminase from Bacillus
RT stearothermophilus, cloning of the corresponding gene, aspcC, and
RT application in a coupled transaminase process.";
RJ APPL. ENVIRON. MICROBIOL. 62:3794-3799(1996).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL; X93600; E212847; ..
CC PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR
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DR	PFAM; PF00155; aminotran_1; 1.	DR	EMBL; L47709; G1146246; -.
KW	TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.	DR	EMBL; 799115; E1183682; -.
FT	BINDING 237 237 PYRIDOXAL PHOSPHATE (BY SIMILARITY).	DR	SUBTILIST; EG11513; ASPB.
SQ	SEQUENCE 393 AA; 42401 MW; 649AD162 CRC32;	DR	PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
		DR	PFAM; PF00155; aminotran_1; 1.
		KW	TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
		FT	BINDING 237 237 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
		SQ	SEQUENCE 393 AA; 43088 MW; 930F37D6 CRC32;
			Query Match 8.5%; Score 319; DB 1; Length 393;
			Best Local Similarity 22.7%; Pred. No. 1.69e-32;
			Matches 83; Conservative 111; Mismatches 155; Indels 16; Gaps 15;
Db	40 PDFNTPQHILDAAIKAMNEGHTKTPSG-GLPALKKEIIRKFFARDQGLDYEPAEVIIVCVG 98	Db	40 PDFNTPQHILDAAVRSMNEGHTKTPSG-GLAELKKSIAEKFRQDNIEYKPSQIIIVCTG 98
Qy	182 PAFTAVEAEDAAVAARTGQFNCYPAGVGLPAARSAVAEHLISQGVPMLSADDFELTAG 241	Qy	182 PAFTAVEAEDAAVAARTGQFNCYPAGVGLPAARSAVAEHLISQGVPMLSADDFELTAG 241
Db	99 AKHALYTLFQVLLD-EGDEVIIPTPYWVYVPEQVKLAG-GVPVYVEGLEQNHFKITPEQL 156	Db	99 AKHALYTLFQVLLD-BEDEVIPTPYWVYVPEQVKLAGGPKPVYVEGLEENHFKISPEQLK 157
Qy	242 GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAFNRLEVRHF-DLPDKGWEIDDSL 300	Qy	242 GTQAIEVIIPVLAQTAGANILLPRPGYPNYEARAFNRLEVRHFDLPDKGWEIDDSL 300
Db	157 KQATTPR-TKAVIINSNPTGMITYTAEELKALGEVCLAHGLIVDSDEIYEKLYGGAKH 215	Db	158 NATYK-TKAVIINSNPTGMITYTAEELKALGEVCLAHGLIVDSDEIYEKLYGGAKH 216
Qy	301 -ESIAADKNTTAMVILNPNPCGSVSYDHLISKVAEVAKRGLIVIADEVYKLVLSGAPF 359	Qy	301 ESIAADKNTTAMVILNPNPCGSVSYDHLISKVAEVAKRGLIVIADEVYKLVLSGAPFI 360
Db	216 VSIAPSLPAAQVITINGVSKSHMTGWRIGYAA--GPKDIIK-A-M-TDLASH-STS- 268	Db	217 SIAQLSRLKEQTVIINGVSKSHMTGWRIGYAGSE--DIIK-A-M-TNLASH-STS-N 269
Qy	360 IPMGVFG-HI-TPVLSIGLSKSMIVPGWRLGWAVYDPRKILQETKISTITNVLNVST 417	Qy	361 PMGVFG-HIT-PVLSIGLSKSMIVPGWRLGWAVYDPRKILQETKISTITNVLNVST 418
Db	269 NPTSTAQVAAATANGGPOEPV-EQWRQAFQRLNIIDKLVQIFGTCV-KPGCAFYLFEP 326	Db	270 PTSTAQVGAIAANGPSEPL-EMREAFEHRLNTIYAKLIEIFGFCV-KPEGAFYLFPN 327
Qy	418 DPATFQAALPQILENTKEDFFKAIIGLKKESSEICYKQIKENYITCPHPKPGSMFVMV 477	Qy	419 PATFQAALPQILENTKEDFFKAIIGLKKESSEICYKQIKENYITCPHPKPGSMFVMVK 478
Db	327 NARGAAMAGCTVDEFAVALLAEKALVPGSGFGAPDNVRLSVATSLDALETAVERIH 386	Db	328 AKAAQSCGFQVDFVKALLEEKVAIVPGSGFGSPENVRSLSVATSLDLLEAERIKR 387
Qy	478 KL-NLHLEEDDDIDFCCKLAKEESVILCPGSLGMANNVRIITFACVPSSLDGLGRIK 536	Qy	479 LNLHLE-EDDDIDFCCKLAKEESVILCPGSLGMANNVRIITFACVPSSLDGLGRIS 537
Db	387 RF 388	Db	388 FVEKH 392
Qy	537 SF 538	Qy	538 FCORN 542
RESULT 8		RESULT 9	
ID	AAT1_BACSU STANDARD; PRT; 393 AA.	ID	PATA_BACSU STANDARD; PRT; 392 AA.
AC	P53001;	AC	P16524;
DT	01-OCT-1996 (REL. 34, CREATED)	DT	01-AUG-1990 (REL. 15, CREATED)
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)	DT	15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)	DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART).	DE	POTATIVE AMINOTRANSFERASE A (EC 2.6.1.1-).
GN	ASPB.	GN	PATA OR UAT.
OS	BACILLUS SUBTILIS.	OS	BACILLUS SUBTILIS.
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;	OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
OC	BACILLUS.	OC	BACILLUS.
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=168 / MABURG;	RC	STRAIN=168;
RX	MEDLINE; 96349105.	RA	SCANLAN E.; DEVINE K.M.;
RA	SOROKIN A.V., AZEVEDO V., ZUMSTEIN E., GALLERON N., EHRLICH S.D.,	RA	ANTONIEWSKI C.; SAVELLI B.; STRAGIER P.;
RA	SERRA P.;	RL	SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RT	"Sequence analysis of the Bacillus subtilis chromosome region between	RP	SEQUENCE OF 361-392 FROM N.A.
RT	the serA and kds loci cloned in a yeast artificial chromosome.";	RX	MEDLINE; 90094275.
RL	MICROBIOLOGY 142:2005-2016(1996)	RA	ANTONIEWSKI C.; SAVELLI B.; STRAGIER P.;
CC	-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE -> OXALOACETATE +	RT	"The spoIIJ gene, which regulates early developmental steps in
CC	L-GLUTAMATE.	RT	Bacillus subtilis, belongs to a class of environmentally responsive
CC	-!- COFACTOR: PYRIDOXAL PHOSPHATE.	RT	genes."
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).	RT	J. BACTERIOL. 172:86-93(1990).
CC	-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT	CC	-!- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
CC	AMINOTRANSFERASES.	CC	-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC		CC	AMINOTRANSFERASES.
CC		CC	
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DR	EMBL:	AJ222587:	EL181905:	-
DR	EMBL:	Z99111:	E1184990:	-
DR	EMBL:	M29450:	G143632:	-
DR	SUBTILIST:	BG10205:	PATA:	-
DR	PROSITE:	PS00105:	AA_TRANSFER_CLASS_1:	1.
KW	TRANSFERASE:	AMINOTRANSFERASE:	PYRIDOXAL PHOSPHATE.	
FT	BINDING	230	230	PYRIDOXAL PHOSPHATE (BY SIMILARITY).
DR	SEQUENCE	352 AA:	43414 MW:	859AD438 CRC32:

Query Match 8.1%; Score 304; DB 1; Length 392;  
Best Local Similarity 23.8%; Pred. No. 5.95e-30;  
Matches 97; Conservative 103; Mismatches 180; Indels 28; Gaps 24;

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Db      1  MEHLNPKARIEISGTR--KFSNVLVAQHE--VISLTIGOPDFFTHHHVKAAKKAIDEN  57
Qy      138  KDGVLAAATGANNRAIRYKISASQVEKGRPVLPLAHPDGVFPFAFRTAVEADAFAAA  197
Db      58  V-TS-YTPN-AGY-L-ELRQAQVLYMKKADFNDAESEIIITTGAQADAFRTIL-SP  111
Qy      198  VRTGQFCNYPAGVGLPAARSAVAEHLISQGVYMLSDADVLTAGGTQATEVIEIPVLAQTA  257
Db     112  GDEVMIPGIYPGEPPIINCGAKPVIYD--TTSHGFKLARLTEDALTPTKCVVLPPYS  170
Qy     258  GANILLPRGYPNYEARAAENRLEVRHFDLIPDKGWEIDIDSLESTADKNTAMWIINPN  317
Db     171  NPTGVTLSSEELKSIAALLKGRNVFVLSDBIYSELYVDRPHY--SIATYLRDQTIV--INSL  228
Qy     318  NPCGSVSYDHLKSVAEAKRLGTLVIAADEVYKGLVLSGAPFIPMGVGHITPVLISGLS  377
Db     229  SKSHSMTGWRIGTFU--FAPKDI--AKHI-LKVHQY-NVSCASSISOKAL--EAVVINGLDD  281
Qy     378  SKSWIVFGRLGWAVYDPRKILQETKISTSTINYNLSTDPATFQAALPOILENTKED  437
Db     282  AL-IMREQYKKRDYVYDRL--VSMGLDVG-KPSGAFYIFPSIK-SF--QWTS-FFFSMAL  334
Qy     438  FFKAIIGLLESSEICYKIKENKYITCPHKPGSMFVAVKVLNLHLEEDIDDDIDFCCKL  497
Db     335  LEDAGVALVPGSSFSFTGCVYVRLSFACSMDTUREGLDRLEIFVLVKKR  382
Qy     498  AKEESVILTCGFSVLGM--AN--WVRITACVPSSLDQGLGRKIKFSFOCRNK  543

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RESULT	10
ID	AATA_RHIME
AC	Q02635;
STANDARD;	PRT; 400 AA.
DT	01-JUL-1993 (REL. 26, CREATED)
DT	01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE	ASPARTATE AMINOTRANSFERASE A (EC 2.6.1.1) (TRANSMINASE A) (ASPAT).
GN	AATA.
OS	RHIZOBIUM MELLIOTI.
OC	BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
OC	RHIZOBIACEAE; SINORHIZOBIUM.

RN	[1]	SEQUENCE FROM N.A.
RP		MEDLINE: 91210178.
RX		RASTOGI V.K., WATSON R.J.;
RT		"Aspartate aminotransferase activity is required for aspartate
RT		catabolism and symbiotic nitrogen fixation in <i>Rhizobium meliloti</i> ."
RL		J. BACTERIOL. 173:2879-2887(1991).
RL	[2]	
RN		SEQUENCE FROM N.A.
RP		RC STRAIN-JJJC10;
RC		MEDLINE: 93209934.
RA		WATSON R.J., RASTOGI V.K.;
RX		"Cloning and nucleotide sequencing of <i>Rhizobium meliloti</i>
RT		aminotransferase genes: an aspartate aminotransferase required for
RT		symbiotic nitrogen fixation is atypical.";
RT		

```

J. BACTERIOL. 175:1919-1928(1993).
-!- FUNCTION: REQUIRED FOR ASYMMETRIC NITROGEN FIXATION.
-!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE + L-GLUTAMATE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.

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-----
EMBL; L05064; GI521149; -.
PIR; A47094; A47094.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
PFAM; PF00155; aminotran_1; 1.
TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
BINDING 239 239 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 400 AA; 443582 MW; 7DD47F70 CRC32;

```

Query Match 7.7%; Score 287; DB 1; Length 400;  
Best Local Similarity 24.7%; Pred. No. 4.29e-27;  
Matches 96; Conservative 85; Mismatches 175; Indels 29; Gaps 23;

[illegible]

RESULT	11
ID	ALAT_YEAST STANDARD; PRT; 507 AA.
AC	P52892;
DT	01-OCT-1996 (REL. 34, CREATED)
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE	PUTATIVE ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).
GN	YDR111C OR YD9727.07C.
OS	SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC	EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES; [1]
CC	SACCHAROMYCETACEAE; SACCHAROMYCES.
RN	
RP	SEQUENCE FROM N.A.
RC	STRAIN-S288C / AB972;

```
-- L-GLUTAMATE.
-- COFACTOR: PYRIDOXAL PHOSPHATE.
-- SUBCELLULAR LOCATION: MITOCHONDRIAL (POTENTIAL).
-- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
-----
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-----
CC      DB    DR   KW  FT     FT     FT     FT     FT     FT     FT     FT     FT     RT
EMBL; U53880; G1256891; -
DR      EMBL; Z73261; E245543; --
KW      HYPOTHETICAL PROTEIN; TRANSFERENCE; AMINOTRANSFERASE;
PYRIDOXAL PHOSPHATE; MITOCHONDRION; TRANSIT PEPTIDE.
FT       TRANSIT          ?           MITOCHONDRION (POTENTIAL)
FT       CHAIN            ?           PUTATIVE ALANINE AMINOTRANSFERASE,
                                     MITOCHONDRIAL.
FT       BINDING         412  412     PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT       SEQUENCE        592 AA; 66421 MW; 5769BA88 CRC32;
Query Match              7.7%; Score 289; DB 1; Length 592;
Best Local Similarity 31.7%; Pred. No. 1.98e-27; Indels 7; Gaps 4;
Matches                   52; Conservative                    51; Mismatches 54;
DB      DQ      YS      SGOGEGRKSAVAEITKRDEIGSPEDIFDTAGASAAVNVLLSFRCGPETGVLP 280
YQ      P06 VPAVGVLPAARSVAEHLSQGVPWMLS-ADDFLTAGGTQAIEVIPVLAQTGANILLP 264
                                         : ::::: | ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
DB      DQ      IPOXYPLATLATLNNSQLPVYLDSNGSTNPBEIIVTVKEAONEKTPIVVVINFGN 340
YQ      P06 ||||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
265 RPGYPNYEARAAFNRLVRHFDLPDKGWEI---DIDSL--ESI-AKDNTAMVIINPN 318
                                         : ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
DB      C41 PTGAVLPSPESTAOFEEAVAKYGVTGVIADEVQEYNIPFCGTKFSM 384
YQ      P06 ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
319 PCGSVISVDHLKSVAEVAKRGILVIDEYVKLVGSAPFIM 362
                                         : ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
RESULT 13
ID XJG0.YEAST STANDARD; PRT: 444 AA.
AC P47039;
DT 01-NOV-1995 (REL. 32, CREATED)
DI 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DD 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOCHRETIMIC AMINOTRANSFERASE YJLO6OW (EC 2.6.1.-).
GN YJLO6OW OR JLI138.
OS SACCHAROMYCES CREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HELMIASCOPHYTES; SACCHAROMYCETALES;
OC OC SACCHAROMYCETACEAE; SACCHAROMYCETES.
RN [1]
RP SEQUENCE FROM N.A.
RA POHL T.M., ALJINOVIC G.;
RL SUBMITTED (SEP-1995), TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [2]
RP SEQUENCE OF 92-222 FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE; 95400292.
RA MASUKAMI Y., NAITO M., HAGIWARA H., SHIBATA T., OZAWA M.,
RA SASAHARA S., SASANOUMA M., TSUCHIDA Y., SOEDA E., YOKOIAMA K.,
RA YANAZAKI M., TASHIRO H., EKII T.;
RT "Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae.";
NL CAT. GENER. 10:261-268(1995).
CC --- COFACTOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
CC --- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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Qy	206	YPAGVGLPAARSVAHEH-SQ-GYFYMLSADDDVFLTAGTQAI-EVILPVLAQTAGANIL	2623
Dd	130	IFPPYWTYSVDIVQICEGKPIILIACDASSGFRLTAAQKLEAAITPTRRWLVLSFNSPSGA	1899
Qy	263	LPRFGYPNTEARAENRLEVRHFOLIPDKGEWIDISLESIAADKNTTAMVLINPNPCGS	3222
Dd	190	AYSAAADYRPLDLVLLKHPHWLVLDDMYEHIVYDAFRFTPARLEPGKDKRTLTVNGVSK	2495

Fri Oct 1 16:47:09 1999

QY 323 VYSYDHLKVAEVA-KRLGILVIADVEYKLVLSAPFFIPMGVFGH-IT-PVLSIGSLSK 379  
Db 250 AYAMTCWRIGYAG--GPR-AL--IK-AMAVVOSQATSC-PSSVSQAASVAALNGP-ODEL 301  
QY 380 SWIVPGWRLGWAVYDPRKILQETKISTITNYLVNSTDPATFIQAALPQILENTKEDEF 439  
Db 302 KERTESFORRNVLVNGLNAIEGLDC-RVPEGAFYTFSGCAGVARRVTPSGKRIESDIDF 360  
QY 440 KATIGLKESESEICYKOIRENKYITCPRPEGSMFVNVK-LNL--HEL--EE-IDDDIDF 493  
Db 361 CAYLLEDHVAVVPVGSAGLSFYRISYATSEAEKLEALERISAACKR 408  
QY 494 CCKLAKEESVILCPGSLGMANWVRITFACVPSSLQDGLGRIKSFQOR 541

Search completed: Fri Oct 1 13:53:55 1999  
Job time : 22 secs.

(TM)

Result No.	score	Query		Length	DB	ID	Description	Pred. No.
		Match	%					
1	1286	34.3	389	1	Q9451		TYROSINE TRANSAMINASE- F42D1.2 PROTEIN.	4.36e-206
2	746	19.9	464	5	O93703		ASPARTATE AMINOTRANSFERSE	2.12e-106
3	489	13.0	429	2	O3267		ASPARTATE AMINOTRANSFERSE	1.84e-60
4	466	12.4	402	2	O86587		ASPARTATE AMINOTRANSFERSE	1.91e-56
5	457	12.2	401	1	O59044		401AA LONG HYPOTHETICA	7.01e-55
6	433	11.5	404	2	P71348		ASPARTATE AMINOTRANSFERSE	1.00e-50
7	415	11.1	402	2	O88124		POTATIVE AMINOTRANSFERSE	1.26e-47
8	402	10.7	394	2	O67781		ASPARTATE AMINOTRANSFERSE	2.13e-45
9	399	10.6	405	2	P77727		FROM BASES 2401667 TO	6.94e-45
10	359	9.6	397	2	O53870		POTATIVE AMINOTRANSFERSE	4.21e-38
11	355	9.5	357	2	O05237		HYPOTHETICAL 39.5 KD P	1.98e-37
12	357	9.5	397	2	O60013		ASPARTATE AMINOTRANSFERSE	9.14e-38
13	353	9.4	390	2	O25383		SOLUTE-BINDING SIGNATU	4.29e-37
14	337	8.0	382	2	O54170		AMINOTRANSFERASE.	2.03e-34
15	323	8.6	379	1	O28151		ASPARTATE AMINOTRANSFERSE	4.29e-32
16	323	8.6	391	1	O58489		391AA LONG HYPOTHETICA	4.29e-32
17	296	7.9	400	2	O64559		POTATIVE ASPARTATE AMI	1.16e-27
18	294	7.8	374	1	O27916		ASPARTATE AMINOTRANSFERSE	2.46e-27
19	283	7.5	383	2	O33822		ASPARTATE AMINOTRANSFERSE	1.49e-25
20	272	7.3	389	1	O59092		389AA LONG HYPOTHETICA	8.74e-24

[illegible]

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Db 189 PGIEAMADENTVAMVIINPNPCGVSYDHLKKVAETAATKGLMWITDEVYQOTIFGDK 248
      ::::: || || || || || || || || || || || || || || || || || || || ||
QY 298 DSLESIAKNTTAMVIINPNPCGVSYDHLKSKVAEAKRLGILVLADEVYKGLVLSA 357
      ::::: || || || || || || || || || || || || || || || || || || || ||
Db 249 PFVPMGFSSITPVITLGGTSGKWIQWGRIGWLTALNDPRGILKSTGCVOSIQOQNLDITP 308
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 358 PFIPMGVFGHTPVLSIGSLSKSWIPGWLGVAVDPRKIQETKISITNLYNVST 417
      ||::|| |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 309 DATIVQAALPEILGKANKELFAKNSMLKONVELCDRLKEIPCLVNCNKKPESCTYLLV 368
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 418 DPATFIAQALPOILENTKEDEFAIGLLKESSEICYKQIKENKYITCPHKPEGSMEVMV 477
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 2
ID Q93703 PRELIMINARY; PRT; 464 AA.
AC Q93703;
DT 01-FEB-1997 (TREMREL. 02, CREATED)
DT 01-FEB-1997 (TREMREL. 02, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMREL. 09, LAST ANNOTATION UPDATE)
DE F42D1.2 PROTEIN.
GN F42D1.2.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RA LIGHTNING J.;
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
RA BONFIELD J., BURTON J., CONNELL M., COPEY T., COOPER J., FULTON L.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., JIER M., JOHNSTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).
DR EMBL; 281081; E1346662; -.
SQ SEQUENCE 464 AA; 51031 MW; A2E3EAB3 CRC32;

Query Match 19.9%; Score 746; DB 5; Length 464;
Best Local Similarity 30.5%; Pred. No. 2.12e-106;
Matches 127; Conservative 126; Mismatches 146; Indels 18; Gaps 17;

Db 45 VLPOSASHKNTVNPYR-KIADACAVPPHPEKKVILHLGDPVSGGKLPPSEIAVOAMHES 103
      ||::: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 141 VLAATG-AMNSIRAIKIS-A-SVOEKGRPVLPPLAHGDPVFPFAFRTAVEADAVAA 197
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 104 VSHMFDGYPAGVALAAREAIERYZS-SADNVFTADDVYLAGSCSHALQMAIEAVAN-A 161
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 198 VRTGQFNCYPAGVGLPAARSAAVHLSQGVPPYMLSADDFVLTAGGTQAIETVPIVLAQTA 257
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 162 GENILVPHGFPLYSTLCRPHNVDPKYIDMTGEDVR-IDLSYMATIIDDDTKALIIVNN 220
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 258 GANILLPRGYPNYEAR-AAFNRLVRH-FDLIPDKGWEIDSLSESIAKNTAMVIN 315
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 221 PGNPTGGVTKHELEILAFAHQYKLIITADEIYGLDLYNGATFYPLASLPKVPITCD 280
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 316 PNPCCSVSYDHLKSKVAEAKRLGILVLADEVYKGLVLSAFPFPMPGVFGHTPVLSIG 375
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 281 GIARKRMVPGWRIGWLIHNFGLVDVKNGI-VALSQKI-VGPCSLVQALPKILRETP 338
      ::::: || || || || || || || || || || || || || || || || || || || ||
QY 376 SLKSKWIPGWRIGWLVAVDPRKIQETKISTITNLYNVSTDPATFIAQALPOILENTK 435
      ::::: || || || || || || || || || || || || || || || || || || || ||
Db 339 EDYFVYTRNVIETNANIVSDILADVPGRMV-RPKGAMVMWNIS-R--TAYGSDVSFCQ 394

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QY 436 EDFFKAILGLLKESSSEICYKQIKENKYITCPHKPEGSMEVMVKLNHLLEEDDDDFCC 495
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 395 NLIRESVP-CLPGQAFSAPGFRVVLTCGSEDEEAALRIRFEFCYRNTHQHSDESD 450
      ::::: || || ::::: || ::::: || ::::: || ::::: || ::::: || ::::: ||
QY 496 KLAKEESVILC-PGSVLGMANVVRITFACVPFSLQDGLGRKIKSCORN-KRNSDD 550
      ::::: || || ::::: || ::::: || ::::: || ::::: || ::::: || ::::: ||

RESULT 3
ID Q33267 PRELIMINARY; PRT; 429 AA.
AC Q33267;
DT 01-JAN-1998 (TREMREL. 05, CREATED)
DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE.
GN MTCY279.04C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORYNEBACTERIINAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA OLIVER K., HARRIS D.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96181548.
RA PHILIPP W.J., POULERT S., EIGLMEIER K., PASCOPELLA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RT "An integrated map of the genome of the tubercle bacillus,
RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
RT leprae.";
RT PROC. NATL. ACADE. SCI. U.S.A. 93:3132-3137(1996).
DR EMBL; 297991; E330321; -.
DR PFAM; PF00155; aminotran.1.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 429 AA; 47350 MW; 9B68011A CRC32;

Query Match 13.0%; Score 489; DB 2; Length 429;
Best Local Similarity 28.6%; Pred. No. 1.84e-60;
Matches 104; Conservative 93; Mismatches 150; Indels 17; Gaps 17;

Db 41 IRGPVHQHAARLEAECHR-ILKLNIGNPAPF-GREAPDVIMRDIQALPYAGYSDSOGI 98
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 151 IRAIRYKISASVQEKGRPRVLPPLAHGDPVFPFAFRTAVEADAVAAVTRTQFNCYPAGV 210
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 99 -LSARRAVYRYVELVPGFP-RFDVDDVYLGNGVSELTITMTLQALDN-GDQVLIPSPDP 155
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 211 GLPAARSVAEH-LSQGVPPYMLSDDFLTAGGTQAEIVIPVLAQTAGANILLPRGYP 269
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 156 LWTASTSAGGTPVHY-LCDETQGHQPIADLESKITER-TKALVVVNNPNTGAVYSCE 213
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 270 NYEARAFNRLEVRHFDLIPDK-GWEIDIDSLSES-IADKNTAMVVIINPNPCGVSYD 327
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 214 ILTQVMDLARKHQLLLADLADIEYDKILYDDAKHISLASIAPDMCLTFLNGLSKAYVAGY 273
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 328 HUSKVAEAKRLGILVLADEVYKGLVLSAFPFPMPGVFGHTPVLSIGLSKSWIPGWR 387
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 274 AGWLAITGPKHEASSFIEGIGILLANRLCPNVPQAHOAIOALGG-HQST-EDLVLPGRRL 331
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 388 LGWVAVDPRKILQETKISTITNLYNVSTDPATF-IOAALPOILENTKEDEFFKAILGL 445
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 332 L-EQRDIATKLNELPGVSCV-KPAGALYAFRLDPEVYD-IDDDQLVLDLLSEKILV 388
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 446 LKESSEICYKQIKENKYITCPHKPEGSMEVMVKLNHLLEEDDDDFCCKLAKESVIL 505

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Db 389 TQGT 392
QY 506 CPGS 509

RESULT 4
ID 086587 PRELIMINARY; PRT; 402 AA.
AC 086587;
DT 01-NOV-1998 (TREMREL. 08, CREATED)
DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)
DE PUTATIVE AMINOTRANSFERASE.
GN SC2H4.04C.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA OLIVER K., HARRIS D.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA PARKHILL J., BARELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE: 97000351.
RA KINASHI H., HOPWOOD D.A.;
RA REDENBACH M., KIESER H.M., DENAPALTE D., EICHNER A., CULLUM J.,
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.
RL MOL. MICROBIOL. 21:77-96(1996).
DR EMBL: AL031514; E1319222.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 402 AA; 44448 MW; 185FB18E CRC32;

Query Match 12.4%; Score 466; DB 2; Length 402;
Best Local Similarity 27.2%; Pred. No. 1.91e-56;
Matches 105; Conservative 107; Mismatches 155; Indels 19; Gaps 17;

Db 24 ANALEEAG-HSVLRINTGNPALF-GFEAPEIVQDMIRMLPRAH-G-YTDSRGILSARRA 79
QY SASVOEKGRPVLPVLAHGDPSPVFAFTAVEADAFAAATGQFCNCPAGVGLPAARSA 218
Db 80 VAQRY-QALGLEVDVDDVFLGNGVSELSMAVQALLE-DCDEVLLPAPDFELTAVTTLA 137
QY VAEHLSQGVPTMLSDADVFLTAGTQAEVLPVLAQTAGANILLPRGYPNEYEARAFN 278
Db 138 GKAVHY-LCDEQAEWYPDLADMEAKITDR-TKAVIINPNPTGAVYKPEIVEGILDLA 195
QY RLEVRHFDLPDKG-WEIDIDSL- IADKNTAMVINPNPGSVSYDHLKVAEVA 336
Db 196 RHGLMWLADIIYQILYDDAVHISAASLAPDLVLLFCGLSKTYRVAGFRSGLWVYTP 255
QY KRGLILVIADEVYKVLGSAFFTPMGVFGHITPVLISGLSKRSWIVPGWRLGWAVYDP 396
Db 256 KOHARDYLEGTLMLASRLCANAPQAQIAOALGGR-QSIRE--LTAPGGLRHEQRDVAW 312
QY RKILQETKISTSIYNLVSTP-PATF-IQALPQILENTKEDFFKAIIGLLESSEICY 454
Db 313 EKLNEIGISCV-KPGKALYAFPRID-PAVHKIHDDERFVLDLILLREKIQVQGTGFNWP 370
QY KQIKENYITCPHKPEGSMEFVWKLNLHLEEDDDDFCCCKLAKESVILCPGSLVGL-- 512
Db 371 SPDHFRLTLPHADLEAAIGRGRF 396
QY MANWVRITFACVPSLQDGLGRKSF 538

RESULT 5
ID 059044 PRELIMINARY; PRT; 401 AA.
AC 059044;
DT 01-AUG-1998 (TREMREL. 07, CREATED)
DT 01-AUG-1998 (TREMREL. 07, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMREL. 09, LAST ANNOTATION UPDATE)
DE 401AA LONG HYPOTHETICAL ASPARTATE AMINOTRANSFERASE.
GN PH1322.
OS PYROCOCUS HORIKOSHII.
OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE: 98344137.
RA KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOIYAMA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTURA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
RA KIKUCHI H.;
RT "Complete Sequence and Gene Organization of the Genome of a
RT Hyper-thermophilic Archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA RES. 5:55-76(1998).
DR EMBL: AP000006; D1031371.
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 401 AA; 45564 MW; 01CD3533 CRC32;

Query Match 12.2%; Score 457; DB 1; Length 401;
Best Local Similarity 29.0%; Pred. No. 7.01e-55;
Matches 93; Conservative 83; Mismatches 132; Indels 13; Gaps 12;

Db 28 LEKKGIK-VIRLNIQDPVAF-DFQPEHMKAEYCAIOEGH-NYYGDSEGLTELREAIK 84
QY 162 VQEKGRPVLPVLAHGDPSPVFAFTAVEADAFAAATGQFCNCPAGVGLPAARSAVAE 221
Db 85 RKEKNGVDITDDVVRVTAATEALQIFGALLD-PGDEILIPGPSYPPTGLVKFYGGK 143
QY 222 HLSQGVPTMLSDADVFLTAGTQAEVLPVLAQTAGANILLPRGYPNEYEARAFNRL 281
Db 144 PVEYRTIEEGWQPDIDDLRKKISER-TKAIIVINPNPTGALYDKKIEELINVAGEHD 202
QY 282 VRHFDLPDKGWEIDIDSL-ESIAKNTAMVINPNPGSVSYDHLKVAEYAKRLG 340
Db 203 LVVLSDIYDLMTYEGKHISSP-GSLTKDVPVIMVNGLSKVYFATGRLGYMVFVDEPKL 261
QY 341 ILVIADEVYKVLGSAFFTPMGVFGHITPVLISGLSKRSWIVPGWRLGWAVYDPKRL 400
Db 262 SEVREAIKLAIRICPNTPQGF--AAIAG-LTGSW-DYLKEYMKKLKRRDFYKRLNE 317
QY 401 QETKISTSIYNLVSTP-PATF-IQALPQILENTKEDFFKAIIGLLESSEICYKQIKE 459
Db 318 IPGIS-TTKPGCAFYIFPRIE 337
QY 460 NKYITCPHKPEGSMEFVWKLNL 480

RESULT 6
ID P71348 PRELIMINARY; PRT; 404 AA.
AC P71348;
DT 01-FEB-1997 (TREMREL. 02, CREATED)
DT 01-FEB-1997 (TREMREL. 02, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (ASPC).
GN HI0286.
OS HAEMOPHILUS INFLUENZAE.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
OC HAEMOPHILUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95350630.
RA FLETSCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
RA KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,
RA MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
RA SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M.,

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RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,  
RA UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,  
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,  
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
RA VENTER J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus  
RT influenzae Rd";  
RL SCIENCE 269:496-512(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA L TATISOV R., MUSEGIAN A.R., BORK P., BROWN N.P., HAYES W.S.,  
RA BORDOVSKY M., RUDD K.E., KOONIN E.V.;  
RL CURR. BIOL. 6:279-291(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
RA KERLAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M.,  
RA MCKENNEY K., SHURLEY R., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
RA SCOTT J.D., SHIRLEY R., LIU L.I., GLODEK A., KELLEY J.M.,  
RA WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,  
RA UTTERBACK T.R., HANNA M.C., SPRIGGS T., SAUDEK D.M., BRANDON R.C.,  
RA FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,  
RA GNEHM C.L., McDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
RA VENTER J.C.;  
RL SUBMITTED (JUL-1995) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.;  
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; U32714; G1573250; -;  
DR PFAM; PF00155; aminotran\_1; 1.  
KW TRANSFERASE; AMINOTRANSFERASE.  
SQ SEQUENCE 404 AA; 45160 MW; 8082209D CRC32;  
  
Query Match 11.5%; Score 433; DB 2; Length 404;  
Best Local Similarity 26.1%; Pred. No. 1.00e-50;  
Matches 103; Conservative 106; Mismatches 166; Indels 20; Gaps 19;  
  
Db 17 IRGVPVKEALRLKEGK-TLKNIGNPAPF-GFEAPDEILVDVRLNLSAQ-G-YCDSK 72  
QY 151 IRAIRKISASVQEKGRPVLPVLAHGDPSPVPAFTAVEADAATAAARTGQNCYPAGV 210  
  
Db 73 GLXSARKAIQYQSKGI-LGATVNDYIGNVSELITMAMQALLN-DGDEVLPMPDYP 130  
QY 211 GLPAARSAAVEHL-SQGVPMLSADDVLTAGTQAEIIPVLAQTAGANILLPRGPV 269  
  
Db 131 LWTAAVTLGGKAVHY-LCDEDANWFTIDDIKAKVNAKTAIIVINPNPTGAVYSKEL 189  
QY 270 NYEARAAFNRLVRFHFDLPKG-WEIDIDSLESIAADKNTAMVINPNPCGSVYSYDH 328  
  
Db 190 LQEVETARONNLIITADEYDKILYDGAHHHIAALAPDLLTTLNGLSKAYRVAGFRQ 249  
QY 329 LSKVAEAKRLGILVIADEVYGLVLSAFPIPMGVFHTPVLSTGLSKSWIVPGWRL 388  
  
Db 250 GWMILNGPKHNAKYIEGLDMLASMRICANVPMOHAITQALGY-OSINE-FILPGRL 307  
QY 389 GWAVYDPRKILQETKISTITNVLNSTD-PATF-IQAALPOLIENTKEDFFKAIIGLL 446  
  
Db 308 EQRNKA-YDILTIQPGITCV-KPMGAMYPEKIDVKFN-IHSDKRVLLDLROEKVLLV 364  
QY 447 KESSEICYKIKENKYITCPHKPEGSFMVVKLNHLLEEDIDDDIDFCCKLAKEESVILC 506  
  
Db 365 HGKGFNHSDFHFRIVLPYV-NOLEAATKLARF 398  
QY 507 PGSVILG--MANWYRI-TFACVPSSLQDGLGRIKSF 538  
  
RESULT 7  
ID O88124 PRELIMINARY; PRT; 402 AA.  
AC O88124;  
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PUTATIVE AMINOTRANSFERASE.  
GN STGA.  
OS STREPTOMYCES ANULATUS.  
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;  
OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA TERCERO J.A., ESPINOSA J.C., JIMENEZ A.;  
RT "StgR, a new Streptomyces alboniger member of the LysR family of  
RT transcribed regulators";  
RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR EMBL; AJ006517; E1318411; -;  
DR EMBL; AJ005198; E1318407; -;  
KW TRANSFERASE; AMINOTRANSFERASE.  
SQ SEQUENCE 402 AA; 44414 MW; 5CD3256A CRC32;  
  
Query Match 11.1%; Score 415; DB 2; Length 402;  
Best Local Similarity 27.2%; Pred. No. 1.26e-47;  
Matches 105; Conservative 99; Mismatches 161; Indels 21; Gaps 16;  
  
Db 24 ANALEEAG-HSVLRNLNTGNPALF-GF-EA--PEEIVQDMIRMLPOAHGYTDSRGVLSARR 78  
QY 159 SASVQEKGRPVLPVLAHGDPSPVPAFTAVEADAATAAARTGQNCYPAGVGLPAARS 217  
  
Db 79 AVAQRYQALGLD-EVSVDDVFLGNVSELVTMAVOALLE-DGDEILIPAPDFPLTAVTT 136  
QY 218 AVAEHL-SQGVPMLSADDVLTAGTQAEIIPVLAQTAGANILLPRGPYPNTEARAA 276  
  
Db 137 LSGGRAVHYVCDEAADWYFDLDDMSKITDOTKAVEIINPT--GAVYPKEILEGILDA 193  
QY 277 FRNLRVRFHFDLPDKGWEIDIDSLESIAADKNTAMVINPNPCGSVYSYDHLKVAEVA 336  
  
Db 194 RRHGLMVFADIEYDQILYDDAVHSHVAALAPDLVLTFCGLSKTYRVAGFRGWLVIITGP 253  
QY 337 KRGLGILVIADEVYGLVLSAFPIPMGVFHTPVLSTGLSKSWIVPGWRLGVAVYDP 396  
  
Db 254 ROHARDYLEGLTMLASMRICNAPQAFQALQALGR-OSIRE--LTAPGGAHGEORAW 310  
QY 397 RKILQETKISTITNVLNSTD-PATF-IQAALPOLIENTKEDFFKAIIGLKESEICY 454  
  
Db 311 EKLNEIPGVSCV-KPKGALYAFPRLDPKV-HPIHDEKRVLDLLQEKIQVYVQGTGFNWP 368  
QY 455 KQIKENKYITCPHKPEGSFMVVKLNHLLEEDIDDDIDFCCKLAKEESVILCPGSVLG-- 512  
  
Db 369 RPDHFRILTPHADLDRAISRGRF 394  
QY 513 MANWYRIEACVPSSLQDGLGRIKSF 538  
  
RESULT 8  
ID O67781 PRELIMINARY; PRT; 394 AA.  
AC O67781;  
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)  
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)  
DE ASPARTATE AMINOTRANSFERASE.  
GN ASPCI.  
OS AQUIFEX AEOLICUS.  
OC BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VF5;  
RX MEDLINE; 98196666.  
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,  
RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,  
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;  
RT "The complete genome of the hyperthermophilic bacterium Aquifex  
RT aeolicus";  
RL NATURE 392:353-358(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VF5;  
RX DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,



RA GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,  
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.,  
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR ENBL: AE000766; G2984217;  
KW TRANSFERASE; AMINOTRANSFERASE.  
SQ SEQUENCE 394 AA; 43777 MW; B9D83011 CRC32;

Query Match 10.7%; Score 402; DB 2; Length 394;  
Best Local Similarity 28.2%; Pred. No. 2.13e-45;  
Matches 103; Conservative 95; Mismatches 139; Indels 28; Gaps 26;

Db 42 PDFDPDFKEACIRALRGKTK-YAPSAGIPELREATAEKLLKENKVEYK-PSEIV-VS 98  
QY 182 PAFRTAVEADVAARVTRGQFNCYPAGVGLPAARSVAEHL-SQG-VPYMLSDDDVFLT 239  
Db 99 AGAKMVLFLFMAILDE--GDEVLLPSYWVTPYQIRFFGGVPV-EVPLKKEKGFQSL 155  
QY 240 AGGTQAI-EVILPVAQTAGANILLPRCPYNYEARAF-NRLEYRHFDLIPDKGWEIDI 297  
Db 156 EDVKEKTER-TRAVINSPNPTGAVYEEELKIAECVER-GIFISDECIEFYVG 213  
QY 298 DSL-ESTADKNTAMVIINPNPCGSVSYDHLKVAEV-AKRLGILYIADDEVYGLVIG 355  
Db 214 DAKFVSPASDEVKNITFTVNAFSSYSMTGWRIGYVA-C-P-E--EVAKVIASLNS-Q 267  
QY 356 SAFPIPGVFGH-ITPV-LSIGLSKSWIVPGWGLGWAVYDPKILQETKISTISITNYL 413  
Db 268 SVS-NVTTFAQYAL-EALKNPKSKDFVNMENAFERRRDTAVELSKIPGMVY-KPEG 324  
QY 414 NVSTDPAFTIQ-AALPQILENTKE-DFFKAIIGLLKESSEICYKIKENKYITCPHKPEG 471  
Db 325 AFYIFDPFSAYA-EKLGDDVKLSEFLLEKAKVAVVPGSAGFAGFLRLSYALSEERLVEG 383  
QY 472 SMFVWVKNLHLEEDDDIDFCKLAKESVILCPGSLGMANVVRITFCVPSLQDG 531  
Db 384 IRRK 388  
QY 532 LGRIK 536

RESULT 9 PRELIMINARY; PRT; 405 AA.  
ID P77727;  
AC P77727;  
DT 01-FEB-1997 (TREMBREL. 02, CREATED)  
DT 01-FEB-1997 (TREMBREL. 02, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)  
DE FROM BASES 2401667 TO 2412529  
OS (SECTION 208 OF 400) OF THE COMPLETE GENOME (SECTION 208 OF 400).  
OS ESCHERICHIA COLI.  
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;  
OC ESCHERICHIA.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K-12;  
RA BLATTNER F.R., PLUNKETT G. III, MAYHEW G.F., PERNA N.T.,  
RA GLASNER F.D.;  
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RA AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,  
RA IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,  
RA KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., MAKINO K.,  
RA MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,  
RA NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,  
RA TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.,  
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
DR ENBL: AE000318; G1788527;  
DR EMBL: D90860; G1799660;  
DR PFAM: PF00155; aminotran-1; 1.  
KW TRANSFERASE; AMINOTRANSFERASE.  
SQ SEQUENCE 405 AA; 45517 MW; DF062CD9 CRC32;

Query Match 10.6%; Score 399; DB 2; Length 405;  
Best Local Similarity 26.3%; Pred. No. 6.94e-45;  
Matches 96; Conservative 99; Mismatches 154; Indels 16; Gaps 16;

Db 17 IRGPVLKEAKRLEEBGNK-VLKLNIGNPAPF-GEDAPDEILYDVRNLPTAQ-G-ICDSK 72  
QY 151 IIRAIYKISASVOEKGRPRVPLAHGDSVPFPAFTAVEADEAFAAARVTRGQFNCYPAGV 210  
Db 73 GLYSARKALIMQHYQARGMRDV-TVEDIYIGNGVSELIVQAMQALLNS-GDEMLVPADPYP 130  
QY 211 GLPAARSVAEHL-SQGVPMLSADDDVLTAGGTQAEVIVPVAQTAGANILLPRGYP 269  
Db 131 LMTAVSISSGKAVIY-LCDESSWFFPDLDIRAKITPRTRGIVIIINPNPTGAVISKEL 189  
QY 270 NYEARAAFNRLVRHFDLIPDKG-WEIDIDLESIAKNTAMVIINPNPCGSVSYDHL 328  
Db 190 LMEIVEIARQHNLIIFADEIYDKILYDDAEHSTAPLAPDLITTFNGLSKTYRVAQFRQ 249  
QY 329 LSKVAEAKRLGILYIADDEVYGLKVLGSAFIPMGVFGHITPVLSIGLSKSWIVPGWRL 388  
Db 250 GWMVLNPKKHAKGIEGLEMLASMLRCANVPAQHAQTALGGY-QSISE-FITPG-GR 306  
QY 389 GWAVYDPRKILQETKISTITNLVSTD-PATF-IOAALPQILENTKEDEFFKAIIGLL 446  
Db 307 YQQRNRAWELINDIPGVCV-KPRGALYMEPKIDAKREN-IHDDQKMWLDLFLQEKVLL 364  
QY 447 KESSEICYKQIKENKYITCPHKPEGSMFVWVKNLHLEEDDDIDFCKLAKESVILC 506  
Db 365 QGTAF 369  
QY 507 PGSVL 511

RESULT 10 PRELIMINARY; PRT; 397 AA.  
ID G53870;  
AC G53870;  
DT 01-JUN-1998 (TREMBREL. 06, CREATED)  
DT 01-JUN-1998 (TREMBREL. 06, LAST SEQUENCE UPDATE)  
DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)  
DE PUTATIVE AMINOTRANSFERASE.  
GN MY043.51C  
OS MYCOBACTERIUM TUBERCULOSIS.  
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIACEAE;  
OC ACTINOMYCETALES; CORYNEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RA HAMLIN N., CHURCHER C.M.;  
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RA COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;  
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE; 96181548.  
RA PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,  
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,  
RA COLE S.T.;  
RT "An integrated map of the genome of the tubercle bacillus,  
RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium  
RT leprae";  
RL PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).  
DR EMBL: AL022004; E1254000; -;  
KW TRANSFERASE; AMINOTRANSFERASE.  
SQ SEQUENCE 397 AA; 42209 MW; 447498CB CRC32;

Query Match 9.6%; Score 359; DB 2; Length 397;  
Best Local Similarity 32.5%; Pred. No. 4.21e-38;  
Matches 66; Conservative 51; Mismatches 79; Indels 7; Gaps 7;



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QY 168 RPVLPLAHGDPSPVPAFTAVEADAFAAIVRTGQFNCIPAGVGLPAARSVAEHLSCQV 227
Db 84 GYEVAESOVLTNGGKQAIYFAAAIL-D-PGDEVIVPAPYTWYTPESIRLAG-GVP-VD 139
QY 228 PYMLSADDDVFLTAGTQAI-EVILPVLQAQAGANILLPRPGYNYEARAAFNLEVRHFD 286
Db 140 VVADETGYRVSVEQLAARTERKVVLFVSPNSPTGVSSEADAKAIGEAHGLWL 199
QY 287 LIPD--KGWEIDIDSLIESIADKNTAMVILNPNPCGVSYSYDHLKSKVAEAKRGLIYI 344
Db 200 TDEYEHVLYGEAKFTSLPVLVPAIRKCIIVNGVAKTYAMTGWVGV-I-APQDVIIKA 257
QY 345 ADEYVGLVLGSAPFIPMGVFGH-ITP-VLSIGLSKSWIVPGWGLGWAVVDPKILQE 402
Db 258 ATNLQSHATS-NVSNVAQVAALAAVSNLDV-AEMKAF-DRRRTM-V--KMLNEIDG 311
QY 403 TKISTITNLYNVSTDPAFTQALPOILENTKEDFKAIIGLKSSESEICYKIKENKY 462
Db 312 VFPC-TPEGAYVPSVKELGKIRKPOSSVELAALILDEVEVAVVPGFAFGPGYL 370
QY 463 ITCPKPKPGSMFV--MYK--LNLHLEEI-DDDIDFCCKLAKEESVILCPGSLGMANNV 517
Db 371 RLSYALGDEDLVEGVSRI 388
QY 518 RITFACVPSSLODGLGRI 535

RESULT 13
ID O25383 PRELIMINARY; PRT; 390 AA.
AC O25383;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE SOLUTE-BINDING SIGNATURE AND MITOCHONDRIAL SIGNATURE PROTEIN (ASPB).
GN HP0672.
OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
OC BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;
OC HELICOBACTER.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695;
EX MEDLINE: 97394467.
RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,
RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
RA COTTON M.D., WEIDMAN J.M., FUJII C., BORMAN C., WATTHEY L., WALLIN E.,
RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
RA VENTER J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori [published erratum appears in Nature 1997 Sep
25:389(6649):412].";
RT NATURE 388:539-547(1997).
RL EMBL: AE000580; G2313794; -.
DR TIGR: HP0672; -.
DR PFAM: PF00155; aminotran_1; 1.
KW HYPOTHETICAL PROTEIN.
SQ SEQUENCE 390 AA; 42874 MW; 8AD53859 CRC32;

Query Match 9.4%; Score 353; DB 2; Length 390;
Best Local Similarity 25.8%; Pred. No. 4.29e-37;
Matches 93; Conservative 86; Mismatches 163; Indels 19; Gaps 17;

Db 40 PDFDTPQAIKDAIKALNDG-FTXTPVAGIPPELLKAIKAKKKNLNDYEPNELYNSG 98
QY 182 PAFRTAVEADAFAAIVRTGQFNCIPAGVGLPAARSVAEHLSCQVYMLSDDDVFLTAG 241
Db 99 AKQSLFNAIQALIE-EGDEVIVPFWYTPYELVKYSG-GYSQFIQTDKSHFKITPKQL 156
QY 242 GTQAIEVILPVLQAQAGANILLPRPGYNYEARAAFNLEVRHFDLIPDKG-WEIDIDSL 300
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Db 157 KDALSPK-TKMLILITPSNETGMLYSKAELEVLGEVLKDTKVVWLSDSEIYEKLYV-KGEF 214
QY 301 -ESADKNTAMVILNPNPCGVSYSYDHLKSKVAEAKRGLIYIADIEVYGLVLGSAFF 359
Db 215 VSCAAVSEEMKKRITITIGLSKSVAMTGWGMGAASDKKLKLMNLOSQCTSNINSIT 274
QY 360 IP-MGVFGHIT-PVLSIGLSKSWIVPGWGLGWAVVDPKILQETKISTITNLYNVST 417
Db 275 QMAS-I-VAL-EGLYD-KE--IETMRQAFERCDLAHAKINAIGGLN-ALKPDGAELYEI 327
QY 418 DPATFIQAALPOILENTKEDFFKAIIGLKSSESEICYKIKENKYITCPHKPGSMFVW 477
Db 328 HIG-SLGC--GDSMRFCHELLEKEGVALVPGKAFGLGVYVRLSFACSEEQIEKGIERAR 384
QY 478 KLNHLLLEEDDDIDFCCKLAKEESVILCPGSLGMANNVRIITFACVPSLSQDGLGRIKS 537
Db 385 F 385
QY 538 F 538

RESULT 14
ID O54170 PRELIMINARY; PRT; 382 AA.
AC O54170;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE AMINOTRANSFERASE.
GN SC7H1.11.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA MURPHY L., HARRIS D.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE: 97000351.
RA REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
RA KINASHI H., HOPWOOD D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb streptomycetes coelicolor A3(2) chromosome.";
RL MOL. MICROBIOL. 21:77-96(1998).
DR EMBL: AL021411; E1245740; -.
SQ TRANSFERASE; AMINOTRANSFERASE.
KW SEQUENCE 382 AA; 40860 MW; 9FC8F75A CRC32;

Query Match 9.0%; Score 337; DB 2; Length 382;
Best Local Similarity 25.7%; Pred. No. 2.03e-34;
Matches 79; Conservative 81; Mismatches 134; Indels 13; Gaps 10;

Db 1 MIATPPASRIAEIARRSRPALAPPGAVSLAMGEPD-FPTPTVVQA--AVSA-LREG 56
QY 142 LAATGANNMSIRAIRYKISASVQKEGPRPVLPLAHGDPSPVPAFTAVEADAFAAIVRTG 201
Db 57 HTH-YADQGRLELRALAAALPERPGAMDDDLVTHGATLAALAAV-LATVGPQDRV 114
QY 202 QFNCPAGVGLPAARSVAEHLSCQVYMLSDDDVFLTAGTQAIIEVILPVLQAQAGANI 261
Db 115 VYPEPAYSILYADLVVLAGTVDFTVPLADLHW--DLALAAALP-GAAMIFSNPSPTG 171
QY 262 LLFPRGYPNYEARAAFNLEVRHFDLIPDKGWEIDIDSLIESIADKNTAMVILNPNPCG 321
Db 172 IVHREELEALGKLIDGTDVLVWSDEAVHRLAYPGHPVSALEIESLRGRVTVQTESKT 231
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QY 322 SVSYDHLKSAEVAKRILGILVIADENVYGLVL-GSAPFIPMGVFGHTIPVLSIGSLKS 380
Db 232 YAMTGRVGYLT--CPREVLDAAOVHRTWNGSLNTAVOHAALALDLPDGVGVAMADRY 289
QY 381 WTVPGRWLGWAVYDPKILQET-KISTSYITNVLNVSTDPATFIOALPQILENTKEDFF 439
Db 290 RQRDLV 296
QY 440 KAIIGLL 446

RESULT 15
ID O28151 PRELIMINARY; PRT; 379 AA.
AC O28151;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE (ASPB-2).
GN AF2129.
OS ARCHAEOGLOBUS FULGIDUS.
OC ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
CC ARCHAEOGLOBUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE; 98049343.
RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBECK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BORMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic,
RT sulphate-reducing archaeon Archaeoglobus fulgidus.";
RL NATURE 390:364-370(1997).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
DR EMBL; AF000957; G2648397; -.
DR TIGR; AF2129; -.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
KW HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
KW PYRIDOXAL PHOSPHATE.
SQ SEQUENCE 379 AA; 42699 MW; C0B47C9E CRC32;

Query Match 8.6%; Score 323; DB 1; Length 379;
Best Local Similarity 26.4%; Pred. No. 4.29e-32;
Matches 95; Conservative 95; Mismatches 143; Indels 27; Gaps 20;

Db 42 PDFTPTDFIIEAAYKAMKEGVF-YTPTKGVPELIDAIVEKLRNENGIDVGAENIIIVTPG 100
QY 182 PAFTAVEAEDAAVAVRTGQNCYPAGVGLPAARSVAEHLSCQVPYMLSADDVFLTAG 241
Db 101 AKYAIFAMCMLL-DEGDVEIILL-PSWVSVEA-CIL-MAGAKPVWVPHEGFE-D-API 154
QY 242 GTQAI-EVITPVLQTAGANILLPRPGYPNEYAARAFNRLEVRHFDLIPDKGWEIDIDL 300
Db 155 EDYITNTKMWNTPSNPLGVVPKFLKVRDLADKDLVMSDEIVEKIIIFEGEHS 214
QY 301 ESTADKNTAMVLIINPNPCGSVSYVDHLKSAEVAKRILGILVIADENVYGLVGSAPFI 360
Db 215 LAAMDGLERTITINGFTSYMTGWRIGYAAPE-W-II---KLMNRQSH-SVS-HPT 267
QY 361 PMGVFGHTIPVLSIGSLKSWIVPGWRLLGWAVYDPKILQETKISTSYITNVLNVSTDP 420
Db 268 SFVQYAGVAAL-KGDQSFKEIVEEFRARRDDIMAKL-DEMGIEYAP-PKGAFYLFMNVG 324
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QY 421 TETQAAALPOILENTKEDFFKAIIGLLKESSEICVYKQIKENKYITCPHKPEGSMFVMVKLN 480
Db 325 -R-----DSN-EFCBEFLKREYVALTPGSAGVAVKSWRLSYATSRERIGEEFLSRLEFE 377
QY 481 LHLLEIDDDIDFCCKLAKEESVILCPGSLGMA--NWRITFACVPSSLODGLGRKISF 538

Search completed: Fri Oct 1 13:54:56 1999
Job time : 44 secs.
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